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OM protein - protein search, using sw model
Run on:         May 12, 2006, 21:13:34 ; Search time 185 Seconds
                                        (without alignments)
                                        211.377 Million cell updates/sec
Title:          US-10-063-557-50
Perfect score:  461
Sequence:       1 MERVTLALLLLAGLTALEAN.........HSPVPEKAIPLITPGSATTC 89
Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched:       2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters:      2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries
Database :       A_Geneseq_21:*
                1:  geneseqp1980s:*
                2:  geneseqp1990s:*
                3:  geneseqp2000s:*
                4:  geneseqp2001s:*
                5:  geneseqp2002s:*
                6:  geneseqp2003as:*
                7:  geneseqp2003bs:*
                8:  geneseqp2004s:*
     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
                                SUMMARIES
  No.   Score  Match Length DB  ID                      Description
RESULT 1
ID   AAY66705 standard; protein; 89 AA.
DE   Membrane-bound protein PRO1069.
PN   WO9963088-A2.
PD   09-DEC-1999.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 3;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 2
ID   AAY87258 standard; protein; 89 AA.
DE   Human signal peptide containing protein HSPP-35 SEQ ID NO:35.
PN   WO200000610-A2.
PD   06-JAN-2000.
PA   (INCY-) INCYTE PHARM INC.
  Query Match             100.0%;  Score 461;  DB 3;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 3
ID   AAY85679 standard; protein; 89 AA.
DE   Human kidney disease associated protein SEQ ID 11.
PN   WO200061622-A2.
PD   19-OCT-2000.
PA   (INCY-) INCYTE PHARM INC.
  Query Match             100.0%;  Score 461;  DB 3;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 4
ID   AAU29123 standard; protein; 89 AA.
DE   Human PRO polypeptide sequence #100.
PN   WO200168848-A2.
PD   20-SEP-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 4;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 5
ID   AAB87550 standard; protein; 89 AA.
DE   Human PRO1069.
PN   WO200116318-A2.
PD   08-MAR-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 4;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 6
ID   AAB65228 standard; protein; 89 AA.
DE   Human PRO1069 (UNQ526) protein sequence SEQ ID NO:262.
PN   WO200073454-A1.
PD   07-DEC-2000.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 4;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 7
ID   ABG95875 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein PRO1069.
PN   US2002119130-A1.
PD   29-AUG-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 5;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 8
ID   ABU58499 standard; protein; 89 AA.
DE   Human PRO polypeptide #100.
PN   US2003027272-A1.
PD   06-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 9
ID   ABU88047 standard; protein; 89 AA.
DE   Novel human secreted and transmembrane protein PRO1069.
PN   US2003032127-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 10
ID   ABU84362 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003032112-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 11
ID   ABR66236 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003027278-A1.
PD   06-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 12
ID   ABR65626 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003036159-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 13
ID   ABU99566 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003040070-A1.
PD   27-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 14
ID   ABU58043 standard; protein; 89 AA.
DE   Human PRO polypeptide #75.
PN   US2003027163-A1.
PD   06-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 15
ID   ABU59121 standard; protein; 89 AA.
DE   Novel human secreted or transmembrane protein PRO1069.
PN   US2002132252-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 16
ID   ABU82633 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein PRO1069.
```

PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 17
ID ABU82805 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 18
ID ABU89926 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 19
ID ABR68175 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 20
ID ABU60552 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, #105.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 21
ID ABU96228 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 22
ID ABU92659 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 23
ID ABO08736 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 24
ID ABO02788 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 25
ID ABR74942 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 26
ID ABR94704 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 27
ID ABU13934 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 28
ID ABU85677 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 29
ID ABU98837 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 30
ID ABU98052 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 31
ID ABU91758 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 32
ID ABU89451 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 33
ID ABU86292 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 34
ID ABU67505 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 35
ID ABU80533 standard; protein; 89 AA.
DE Human PRO protein #100.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 36
ID ABU72519 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.

PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 37
ID ABU90900 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 38
ID ABO33959 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 39
ID ABR99451 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 40
ID ABR98841 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 41
ID ABO16364 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 42
ID ABR92264 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 43
ID ABO18905 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 44
ID ABR78326 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 45
ID ABU71976 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 46
ID ABU85062 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 47
ID ABO00201 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 48
ID ABO11533 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 49
ID ABO02178 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 50
ID ABU88752 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 51
ID ABU83447 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 52
ID ABO06248 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 53
ID ABR59284 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 54
ID ABO09346 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 55
ID ABO19210 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 56
ID ABO11228 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.

PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 57
ID ABR66846 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 58
ID ABO16059 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 59
ID ABO13765 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 60
ID ABU71530 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 61
ID ABU65668 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, SEQ ID 200.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 62
ID ABO07516 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 63
ID ABO03703 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 64
ID ABR67151 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 65
ID ABO15754 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 66
ID ABU56035 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, PRO1069.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 67
ID ABU72311 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 68
ID ABU65363 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 69
ID ABU95308 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 70
ID ABU71211 standard; protein; 89 AA.
DE Human PRO1069 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 71
ID ABO07821 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 72
ID ABR70062 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 73
ID ABR69395 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 74
ID ABO01536 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 75
ID ABU81338 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 76
ID ABR60135 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032137-A1.

PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 77
ID ABU90984 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 78
ID ABR67870 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 79
ID ABR65258 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 80
ID ABR68480 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 81
ID ABR71892 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 82
ID ABU59268 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, #105.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 83
ID ABU85372 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 84
ID ABU89062 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 85
ID ABU83142 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 86
ID ABU94998 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 87
ID ABU90546 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 88
ID ABU84057 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 89
ID ABU93708 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 90
ID ABO25965 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 91
ID ABR64953 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 92
ID ABO27305 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO1069.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 93
ID ABR68785 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 94
ID ABO06601 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 95
ID ABR99146 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 96
ID ABU57030 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003027280-A1.
PD 06-FEB-2003.

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  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 97
ID   ABU85982 standard; protein; 89 AA.
DE   Novel human secreted and transmembrane protein PRO1069.
PN   US2003022300-A1.
PD   30-JAN-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 98
ID   ABU82269 standard; protein; 89 AA.
DE   Novel human secreted and transmembrane protein PRO1069.
PN   US2003036136-A1.
PD   20-FEB-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 99
ID   ABU87280 standard; protein; 89 AA.
DE   Human PRO polypeptide #100.
PN   US2003036138-A1.
PD   20-FEB-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 100
ID   ABU83752 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003032109-A1.
PD   13-FEB-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 101
ID   ABO08126 standard; protein; 89 AA.
DE   Human PRO polypeptide #100.
PN   US2003040066-A1.
PD   27-FEB-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 102
ID   ABU92500 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein PRO1069.
PN   US2003045684-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 103
ID   ABU81837 standard; protein; 89 AA.
DE   Novel human secreted and transmembrane protein PRO1069.
PN   US2003032104-A1.
PD   13-FEB-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 104
ID   ABU66001 standard; protein; 89 AA.
DE   Novel human secreted and transmembrane protein PRO1069.
PN   US2003036157-A1.
PD   20-FEB-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 105
ID   ABU81170 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069.
PN   US2003027212-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 106
ID   ABR59830 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003032120-A1.
PD   13-FEB-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 107
ID   ABU94018 standard; protein; 89 AA.
DE   Novel human secreted and transmembrane protein PRO1069.
PN   US2003036155-A1.
PD   20-FEB-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 108
ID   ABU99871 standard; protein; 89 AA.
DE   Novel human secreted and transmembrane protein PRO1069.
PN   US2003022296-A1.
PD   30-JAN-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 109
ID   ABR66541 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003027281-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 110
ID   ABR90959 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003040058-A1.
PD   27-FEB-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 111
ID   ABO53285 standard; protein; 89 AA.
DE   Novel human secreted and transmembrane protein PRO1069.
PN   US2003027986-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 112
ID   ABU58974 standard; protein; 89 AA.
DE   Human sectreted/transmembrane protein, #105.
PN   US2002142961-A1.
PD   03-OCT-2002.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 113
ID   ABU94386 standard; protein; 89 AA.
DE   Human PRO polypeptide #100.
PN   US2003017540-A1.
PD   23-JAN-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 114
ID   ABU79268 standard; protein; 89 AA.
DE   Human PRO polypeptide #100.
PN   US2003032106-A1.
PD   13-FEB-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 115
ID   ABU86597 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003032129-A1.
PD   13-FEB-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 116
ID   ABU86902 standard; protein; 89 AA.
DE   Novel human secreted and transmembrane protein PRO1069.
PN   US2003032131-A1.
PD   13-FEB-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
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  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 117
ID   ABU94691 standard; protein; 89 AA.
DE   Human PRO polypeptide #100.
PN   US2003032103-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 118
ID   ABO04618 standard; protein; 89 AA.
DE   Human PRO polypeptide #100.
PN   US2003032107-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 119
ID   ABR70367 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003032139-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 120
ID   ABU92352 standard; protein; 89 AA.
DE   Novel human secreted and transmembrane protein PRO1069.
PN   US2003022187-A1.
PD   30-JAN-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 121
ID   ABU98532 standard; protein; 89 AA.
DE   Human PRO polypeptide #100.
PN   US2003022301-A1.
PD   30-JAN-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 122
ID   ABR65931 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003036165-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 123
ID   ABR64648 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003027262-A1.
PD   06-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 124
ID   ABU59417 standard; protein; 89 AA.
DE   Novel human secreted or transmembrane protein PRO1129.
PN   US2003027985-A1.
PD   06-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 125
ID   ABU79573 standard; protein; 89 AA.
DE   Human PRO polypeptide #100.
PN   US2003032110-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 126
ID   ABU92964 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003036142-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 127
ID   ABU95923 standard; protein; 89 AA.
DE   Human PRO polypeptide #100.
PN   US2003036145-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 128
ID   ABU91143 standard; protein; 89 AA.
DE   Novel human secreted and transmembrane protein PRO1069.
PN   US2003036154-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 129
ID   ABU90236 standard; protein; 89 AA.
DE   Novel human secreted and transmembrane protein PRO1069.
PN   US2003036153-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 130
ID   ABO09651 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003044931-A1.
PD   06-MAR-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 131
ID   ABO10923 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003036150-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 132
ID   ABR70977 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003040069-A1.
PD   27-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 133
ID   ABU98287 standard; protein; 89 AA.
DE   Novel human secreted and transmembrane protein PRO1069.
PN   US2002183493-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 134
ID   ABU87585 standard; protein; 89 AA.
DE   Human PRO polypeptide #100.
PN   US2003022293-A1.
PD   30-JAN-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 135
ID   ABU91453 standard; protein; 89 AA.
DE   Human PRO polypeptide #100.
PN   US2003032128-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 136
ID   ABU89292 standard; protein; 89 AA.
DE   Novel human secreted and transmembrane protein PRO1069.
PN   US2003036634-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 137
ID   ABU84667 standard; protein; 89 AA.
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DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 138
ID ABR69757 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 139
ID ABU80134 standard; protein; 89 AA.
DE Human PRO protein #100.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 140
ID ABU82499 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 141
ID ABU92183 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 142
ID ABU93403 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 143
ID ABO09956 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 144
ID ABO09041 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 145
ID ABU96463 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 146
ID ABU10889 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 147
ID ABU10609 standard; protein; 89 AA.
DE Human secreted/transmembrane protein #100.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 148
ID ABU81641 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 149
ID ABU72133 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 150
ID ABU95618 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 151
ID ABU96827 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 152
ID ABR70672 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 153
ID ABO05023 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 154
ID ABO08431 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 155
ID ABU88580 standard; protein; 89 AA.
DE Human secreted and transmembrane polypeptide PRO1069.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 156
ID ABO34094 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;

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  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 157
ID   ABO05638 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003032118-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 158
ID   ABR74027 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003036135-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 159
ID   ABR95619 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003054455-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 160
ID   ABR80916 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003049741-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 161
ID   ABR81221 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003049743-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 162
ID   ABM00917 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003049769-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 163
ID   ABR88519 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003068743-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 164
ID   ABM77340 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003054479-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 165
ID   ABO28824 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003068685-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 166
ID   ABO31569 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003068725-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 167
ID   ABM07986 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003068752-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 168
ID   ABO40466 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003068682-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 169
ID   ABO35891 standard; protein; 89 AA.
DE   Human PRO polypeptide #100.
PN   US2003068701-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 170
ID   ABO44030 standard; protein; 89 AA.
DE   Human PRO polypeptide #100.
PN   US2003068755-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 171
ID   ADA77952 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003073180-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 172
ID   ABM24825 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003104539-A1.
PD   05-JUN-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 173
ID   ABO03093 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003036131-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 174
ID   ABR90349 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003040075-A1.
PD   27-FEB-2003.
  Query Match             100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4e-50;
RESULT 175
ID   ABM17263 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003054459-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 176
ID   ABR95009 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003044930-A1.
PD   06-MAR-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 177
ID   ABR95314 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003040071-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 178
ID   ADB17107 standard; protein; 89 AA.
DE   Human transmembrane PRO polypeptide (SeqID 50).
PN   US2003050462-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 179
ID   ABO21552 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003054471-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 180
ID   ABR97816 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003064452-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 181
ID   ABR87604 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003068705-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 182
ID   ABM77645 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003054473-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 183
ID   ABM27875 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003064440-A1.
PD   03-APR-2003.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 184
ID   ABM06156 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003068704-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 185
ID   ABM03662 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003068722-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 186
ID   ABM35113 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003073183-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 187
ID   ABM26350 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003104549-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 188
ID   ABO48132 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003049749-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 189
ID   ABR92874 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003064462-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 190
ID   ABO24635 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein (PRO) #100.
PN   US2003065159-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 191
ID   ADA37773 standard; protein; 89 AA.
DE   Human secreted/transmembrane protein PRO1069.
PN   US2003008297-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 192
ID   ABM11646 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003064447-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 193
ID   ABM02747 standard; protein; 89 AA.
DE   Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN   US2003073184-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 461;  DB 6;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 4e-50;
RESULT 194
ID   ABM16043 standard; protein; 89 AA.
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DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 195
ID ABO27604 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 196
ID ABM29095 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 197
ID ABM07071 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 198
ID ABM21165 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 199
ID ABM09511 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 200
ID ABO41381 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 201
ID ABO36196 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 202
ID ABO43725 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 203
ID ABM76425 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 204
ID ABM76121 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 205
ID ABM25740 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 206
ID ABM26045 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 207
ID ADA21459 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO1069.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 208
ID ABO03398 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 209
ID ABO02483 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 210
ID ABO44263 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO 1069.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 211
ID ABR90654 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 212
ID ABR73722 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 213
ID ABO16974 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.

PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 214
ID ABR94399 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 215
ID ABR75906 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 216
ID ABR71282 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 217
ID ABR93179 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 218
ID ABR93484 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 219
ID ADA10246 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, PRO1069.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 220
ID ABR87909 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 221
ID ABO27909 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 222
ID ABO30044 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 223
ID ABO33253 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 224
ID ABM04941 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 225
ID ABM08901 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 226
ID ABO36501 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 227
ID ABO35586 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 228
ID ABO39551 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 229
ID ABM10426 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 230
ID ABM11951 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 231
ID ABO52097 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 232
ID ABO52402 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 233
ID ADA19912 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 234
ID ABO23720 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 235
ID ADB17295 standard; protein; 89 AA.
DE Human transmembrane PRO polypeptide (SeqID 50).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 236
ID ADA17790 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 237
ID ABR97206 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 238
ID ABR86994 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 239
ID ABM11036 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 240
ID ABM28180 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 241
ID ABO32179 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 242
ID ABM15306 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 243
ID ABM06461 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 244
ID ABM04272 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 245
ID ABM22385 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 246
ID ABM07681 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 247
ID ABO40771 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 248
ID ABM35418 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 249
ID ABM33181 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 250
ID ABO52707 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049773-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 251
ID ABO50267 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 252
ID ABU99261 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 253
ID ABO04313 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 254
ID ABO05943 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 255
ID ABM18483 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 256
ID ADA27898 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 257
ID ABR97511 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 258
ID ABR80611 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 259
ID ABM01222 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 260
ID ABR88824 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 261
ID ABM13476 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 262
ID ABM20860 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 263
ID ABO41991 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 264
ID ABO42601 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 265
ID ABM10121 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 266
ID ABO38636 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 267
ID ABM32876 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 268
ID ABM22690 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 269
ID ABM74901 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003096353-A1.
PD 22-MAY-2003.

Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 270
ID ADA79744 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 271
ID ABR96291 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 272
ID ABM02442 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 273
ID ABR86384 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 274
ID ABR86689 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 275
ID ABM16653 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 276
ID ABM29705 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 277
ID ABO29129 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 278
ID ABM23910 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 279
ID ABM23300 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 280
ID ABM22080 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 281
ID ABO37721 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 282
ID ABM28485 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 283
ID ABM28790 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 284
ID ABM66434 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 285
ID ABM75816 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 286
ID ABM34096 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 287
ID ABM34401 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 288
ID ABO20332 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032125-A1.

PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 289
ID ABO21247 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 290
ID ABO22162 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 291
ID ADA20084 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 292
ID ABO34191 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO 1069.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 293
ID ABR96596 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 294
ID ADA94478 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 295
ID ABR85774 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 296
ID ABR99756 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 297
ID ABM00612 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 298
ID ABM00307 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 299
ID ABO29739 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 300
ID ABM23605 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 301
ID ABM29400 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 302
ID ABO38331 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 303
ID ABO45631 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 304
ID ABM20555 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 305
ID ADA81471 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 306
ID ABO16669 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 307
ID ABO18295 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044920-A1.

PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 308
ID ABO22722 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 309
ID ABO23027 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 310
ID ABR92569 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 311
ID ABR81526 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 312
ID ABM77950 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 313
ID ABR89739 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 314
ID ABM26655 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 315
ID ABM13781 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 316
ID ABO28519 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 317
ID ABO30349 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 318
ID ABM07376 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 319
ID ABM03967 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 320
ID ABO37111 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 321
ID ABO41686 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 322
ID ABO35281 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 323
ID ABM25130 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 324
ID ABO47522 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 325
ID ABO47827 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 326
ID ABO48437 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.

PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 327
ID ABO51487 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 328
ID ABO51792 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 329
ID ABO50572 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 330
ID ABR79696 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 331
ID ABM16958 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 332
ID ABO17990 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 333
ID ABO20942 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 334
ID ABR96901 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 335
ID ADA38703 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 336
ID ABM12256 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 337
ID ABM16348 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 338
ID ABM24215 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 339
ID ABM14696 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 340
ID ABM04577 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 341
ID ABM06766 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 342
ID ABM09206 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 343
ID ABO39246 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 344
ID ABM75511 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 345
ID ABM25435 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.

PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 346
ID ABM19945 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 347
ID ABO46851 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 348
ID ABO47156 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 349
ID ADA83269 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 350
ID ABR71587 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 351
ID ABR72197 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 352
ID ABR98536 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 353
ID ABO06906 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 354
ID ABR84859 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 355
ID ABR73417 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 356
ID ABR76511 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 357
ID ABR73112 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 358
ID ABM18178 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 359
ID ABO20637 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 360
ID ABO25380 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 361
ID ABO25685 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 362
ID ABR94094 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 363
ID ADA92824 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 364
ID ABR80001 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 365
ID ABM11341 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 366
ID ABO32948 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 367
ID ABO30654 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 368
ID ABO30959 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 369
ID ABM27265 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 370
ID ABM30010 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 371
ID ABM05546 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 372
ID ABM15611 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 373
ID ABM08596 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 374
ID ABO42296 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 375
ID ABO38026 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 376
ID ABO45936 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 377
ID ABM66739 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 378
ID ADB20312 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 379
ID ABM19640 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 380
ID ABO49352 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 381
ID ABO49657 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 382
ID ADA78564 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 383
ID ABR88214 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.

PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 384
ID ADA00381 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO 1069.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 385
ID ABM26960 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 386
ID ABM03357 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 387
ID ABO39856 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 388
ID ABO49962 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 389
ID ABO50877 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 390
ID ABO05333 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 391
ID ABR74637 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 392
ID ABR77116 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 393
ID ABM17873 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 394
ID ABR95924 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 395
ID ABO21857 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 396
ID ABO20027 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 397
ID ABO24330 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 398
ID ABR86079 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 399
ID ABM10731 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 400
ID ABM76730 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 401
ID ABR89434 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 402
ID ABM12561 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073176-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 403
ID ABM05851 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 404
ID ABO34976 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 405
ID ABM03052 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 406
ID ABM19030 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 407
ID ABM19335 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 408
ID ABO46546 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 409
ID ABO49047 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 410
ID ABR69090 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 411
ID ABR89129 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 412
ID ABR72502 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 413
ID ABR74332 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 414
ID ABO18600 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 415
ID ABR80306 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 416
ID ABM01527 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 417
ID ABM02137 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 418
ID ABR87299 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 419
ID ABM12866 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 420
ID ABM30620 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 421
ID ABM24520 standard; protein; 89 AA.

DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 422
ID ABO29434 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 423
ID ABO31264 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 424
ID ABM14391 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 425
ID ABM09816 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 426
ID ABO38941 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 427
ID ABM34706 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 428
ID ABO51182 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 429
ID ABO04008 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 430
ID ABO10478 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 431
ID ABO53180 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 432
ID ABR77721 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 433
ID ABR78931 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 434
ID ABO24025 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 435
ID ABR93789 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 436
ID ABM01832 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 437
ID ABM78255 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 438
ID ABR90044 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 439
ID ADA22385 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO1069.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 440
ID ABM27570 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.

PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 441
ID ABM13171 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 442
ID ABO31874 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 443
ID ABM14086 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 444
ID ABM08291 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 445
ID ABO40161 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 446
ID ABM74596 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 447
ID ABM33791 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 448
ID ABM20250 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 449
ID ABO48742 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 450
ID ABO22550 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 451
ID ABR72807 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 452
ID ABO15449 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 453
ID ABR85164 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 454
ID ABO15144 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 455
ID ABO17279 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 456
ID ABM17568 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 457
ID ADA06551 standard; protein; 89 AA.
DE Human secreted/transmembrane PRO polypeptide #75.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 458
ID ADA39244 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 459
ID ABR85469 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 460
ID ABM77035 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 461
ID ABO28214 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 462
ID ABM22995 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 463
ID ABM30315 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 464
ID ABM21775 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 465
ID ABM21470 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 466
ID ABM15001 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 467
ID ABO41076 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 468
ID ABO36806 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 469
ID ABO37416 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 470
ID ABM75206 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 471
ID ABM33486 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 472
ID ABO46241 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 473
ID ADA82635 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 474
ID ADB85623 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 475
ID ADB96270 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 476
ID ABM31840 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 477
ID ABM31230 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 478
ID ADB85943 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.

PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 479
ID ABM32145 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 480
ID ABM32450 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 481
ID ADB68302 standard; protein; 89 AA.
DE Human PRO1069 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 482
ID ADB68109 standard; protein; 89 AA.
DE Human PRO1069 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 483
ID ABM31535 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 484
ID ABM30925 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 485
ID ADB90926 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 486
ID ADC57742 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 487
ID ADC55106 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 488
ID ADC11973 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 489
ID ADC07006 standard; protein; 89 AA.
DE Human PRO1069 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 490
ID ADC56395 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 491
ID ADC17185 standard; protein; 89 AA.
DE Mammalian PRO polypeptide (SeqID 50).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 492
ID ADC07450 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 493
ID ADC11440 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 494
ID ADC14883 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 495
ID ADC52378 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 496
ID ADC14562 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 497
ID ADD08094 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003068623-A1.

PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 498
ID ADC81919 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 499
ID ADD07561 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 500
ID ADC82452 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 501
ID ADD05673 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 502
ID ADD08632 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 503
ID ADD06881 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 504
ID ADC83128 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 505
ID ADD55235 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 506
ID ADD36054 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 507
ID ADD56193 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 508
ID ADD54631 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 509
ID ADE26785 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 510
ID ADE26252 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 511
ID ADF67189 standard; protein; 89 AA.
DE Human PRO1069 amino acid sequence SEQ ID NO:262.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 512
ID ADG01055 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 513
ID ADG08608 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 514
ID ADG02668 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 515
ID ADG01375 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 516
ID ADF95550 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 517
ID ADF95229 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 518
ID ADG12365 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 519
ID ADH24082 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 520
ID ADH34108 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 521
ID ADH29941 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 522
ID ADH23912 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 523
ID ADH09025 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 524
ID ADG85316 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 525
ID ADH24592 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 526
ID ADH37448 standard; protein; 89 AA.
DE Human secreted and transmembrane protein PRO1069.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 527
ID ADH02037 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 528
ID ADH37618 standard; protein; 89 AA.
DE Human secreted and transmembrane protein PRO1069.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 529
ID ADG85656 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 530
ID ADH24252 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 531
ID ADH38546 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 532
ID ADG83667 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 533
ID ADH29475 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 534
ID ADH27591 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 535
ID ADH37788 standard; protein; 89 AA.

DE Human secreted and transmembrane protein PRO1069.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 536
ID ADH37965 standard; protein; 89 AA.
DE Human secreted and transmembrane protein PRO1069.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 537
ID ADH57385 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 538
ID ADH53527 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 539
ID ADH53697 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 540
ID ADH52033 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 541
ID ADH49888 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 542
ID ADI25398 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 543
ID ADH90191 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 544
ID ADI25568 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 545
ID ADH97742 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 546
ID ADI35443 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 547
ID ADI03590 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 548
ID ADI11947 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 549
ID ADH90021 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 550
ID ADH99935 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 551
ID ADH98422 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 552
ID ADI11097 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 553
ID ADI11607 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 554
ID ADH98252 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 555
ID ADH98592 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 556
ID ADH98082 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 557
ID ADI05070 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 558
ID ADI03420 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 559
ID ADI04815 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 560
ID ADH78269 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 561
ID ADI19613 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 562
ID ADH90361 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 563
ID ADI03080 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 564
ID ADH77929 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 565
ID ADH97912 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 566
ID ADI01297 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 567
ID ADI01992 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 568
ID ADI03250 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 569
ID ADI11437 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 570
ID ADI02339 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 571
ID ADI11777 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 572
ID ADI05414 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 573
ID ADH79486 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 574
ID ADI19443 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 575
ID ADI05244 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 576
ID ADH79656 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 577
ID ADI01482 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 578
ID ADI01652 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 579
ID ADI01822 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 580
ID ADH79826 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 581
ID ADI04644 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 582
ID ADI02780 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 583
ID ADH78099 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 584
ID ADI25738 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 585
ID ADI25908 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 586
ID ADK65420 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 587
ID ADH98762 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 588
ID ADH80003 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 589
ID ADL32806 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 590
ID ADM30340 standard; protein; 89 AA.

DE Novel human secreted and transmembrane protein PRO1069.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 591
ID ADL93734 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 592
ID ADC52188 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 593
ID ADE74337 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 594
ID ADE74949 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 595
ID ADF35388 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 596
ID ADG11638 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 597
ID ADF96162 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 598
ID ADG04433 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 599
ID ADG00593 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 600
ID ADH06620 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 601
ID ADH06450 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 602
ID ADG68871 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 603
ID ADH27761 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 604
ID ADH25102 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 605
ID ADH33734 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 606
ID ADG82849 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 607
ID ADH02377 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 608
ID ADH07984 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 609
ID ADG69381 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 610
ID ADH39202 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 611
ID ADH26130 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 612
ID ADG83942 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 613
ID ADH19508 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 614
ID ADG85486 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 615
ID ADH06280 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 616
ID ADH30110 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 617
ID ADH24422 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 618
ID ADH33099 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 619
ID ADG69551 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 620
ID ADH07814 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 621
ID ADG85826 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 622
ID ADH39372 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 623
ID ADH33564 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 624
ID ADH33904 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 625
ID ADH01114 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 626
ID ADG69721 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 627
ID ADH21001 standard; protein; 89 AA.

DE Human secreted/transmembrane protein PRO1069.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 628
ID ADH02207 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 629
ID ADG69211 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 630
ID ADG85996 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 631
ID ADH24932 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 632
ID ADH39549 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 633
ID ADH20041 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 634
ID ADH02547 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 635
ID ADG69041 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 636
ID ADH07644 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 637
ID ADG86166 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 638
ID ADH24762 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 639
ID ADH25810 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 640
ID ADH38376 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 641
ID ADH57215 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 642
ID ADH52203 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 643
ID ADH49569 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 644
ID ADH90531 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 645
ID ADI11267 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181683-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 646
ID ADH98932 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 647
ID ADI02162 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 648
ID ADH90701 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 649
ID ADJ54838 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 650
ID ADJ98576 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 651
ID ADJ98746 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 652
ID ADH78905 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 653
ID ADJ99139 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 654
ID ADJ99309 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 655
ID ADJ98927 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 656
ID ADH79075 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 657
ID ADK00935 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 658
ID ADK14456 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 659
ID ADJ64609 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 660
ID ADM31505 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 661
ID ADM36552 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 662
ID ADM40357 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 663
ID ADM80905 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 664
ID ADN37965 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 665
ID ADY77745 standard; protein; 89 AA.
DE Neoplastic disease detection protein PRO1069.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 461; DB 9; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 666
ID AEA38515 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, #143.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 9; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 667
ID AAW92958 standard; protein; 89 AA.
DE Human zsig44 protein.
PN WO9905276-A1.
PD 04-FEB-1999.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 98.0%; Score 452; DB 2; Length 89;
Best Local Similarity 98.9%; Pred. No. 5.5e-49;
RESULT 668
ID AAM38770 standard; protein; 89 AA.
DE Human polypeptide SEQ ID NO 1915.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 98.0%; Score 452; DB 4; Length 89;
Best Local Similarity 98.9%; Pred. No. 5.5e-49;
RESULT 669
ID ADK14984 standard; protein; 89 AA.
DE Urinary specific protein #90.
PN WO2003057839-A2.
PD 17-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 98.0%; Score 452; DB 7; Length 89;
Best Local Similarity 98.9%; Pred. No. 5.5e-49;
RESULT 670
ID AAM40556 standard; protein; 117 AA.
DE Human polypeptide SEQ ID NO 5487.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 98.0%; Score 452; DB 4; Length 117;
Best Local Similarity 98.9%; Pred. No. 7.9e-49;
RESULT 671
ID ADP07847 standard; protein; 89 AA.
DE Human secreted protein, seq id 330.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.0%; Score 447; DB 8; Length 89;
Best Local Similarity 97.8%; Pred. No. 2.4e-48;
RESULT 672
ID ADN38892 standard; protein; 186 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:210.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 81.1%; Score 374; DB 7; Length 186;
Best Local Similarity 94.7%; Pred. No. 1.1e-38;
RESULT 673
ID ADN38894 standard; protein; 318 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:212.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 81.1%; Score 374; DB 7; Length 318;
Best Local Similarity 94.7%; Pred. No. 2.2e-38;
RESULT 674
ID AAE05362 standard; protein; 88 AA.
DE Mouse channel inducing factor precursor (CHIF) protein.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 60.0%; Score 276.5; DB 4; Length 88;
Best Local Similarity 66.7%; Pred. No. 9.7e-27;
RESULT 675
ID ABB72374 standard; protein; 88 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 698.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 60.0%; Score 276.5; DB 5; Length 88;
Best Local Similarity 66.7%; Pred. No. 9.7e-27;
RESULT 676
ID AAW92966 standard; protein; 87 AA.
DE Rat CHIF protein.
PN WO9905276-A1.
PD 04-FEB-1999.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 55.6%; Score 256.5; DB 2; Length 87;
Best Local Similarity 61.5%; Pred. No. 3.3e-24;
RESULT 677
ID AAR90991 standard; protein; 88 AA.
DE Mouse Mat-8 polypeptide.
PN WO9605322-A1.
PD 22-FEB-1996.
PA (GEHO) GEN HOSPITAL CORP.
PA (HARD) HARVARD COLLEGE.
Query Match 52.4%; Score 241.5; DB 2; Length 88;
Best Local Similarity 57.8%; Pred. No. 2.7e-22;
RESULT 678
ID AAR90990 standard; protein; 87 AA.
DE Human Mat-8 polypeptide.
PN WO9605322-A1.
PD 22-FEB-1996.
PA (GEHO) GEN HOSPITAL CORP.
PA (HARD) HARVARD COLLEGE.
Query Match 46.5%; Score 214.5; DB 2; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 679
ID AAY48304 standard; protein; 87 AA.
DE Human prostate cancer-associated protein 1.
PN DE19811194-A1.
PD 16-SEP-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 46.5%; Score 214.5; DB 2; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 680
ID AAW92959 standard; protein; 87 AA.
DE Human MAT-8 protein.
PN WO9905276-A1.
PD 04-FEB-1999.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 46.5%; Score 214.5; DB 2; Length 87;

Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 681
ID AAM23962 standard; protein; 87 AA.
DE Human EST encoded protein SEQ ID NO: 1487.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 46.5%; Score 214.5; DB 4; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 682
ID ABJ37036 standard; protein; 87 AA.
DE Human breast cancer / ovarian cancer related protein #12.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 46.5%; Score 214.5; DB 6; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 683
ID ABR47467 standard; protein; 87 AA.
DE Breast cancer associated protein sequence SEQ ID NO:166.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 46.5%; Score 214.5; DB 6; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 684
ID ABP75985 standard; protein; 87 AA.
DE Human GENSET protein SEQ ID 192.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
Query Match 46.5%; Score 214.5; DB 6; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 685
ID ABP76150 standard; protein; 87 AA.
DE Human GENSET protein SEQ ID 476.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
Query Match 46.5%; Score 214.5; DB 6; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 686
ID ADB75316 standard; protein; 87 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 46.5%; Score 214.5; DB 7; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 687
ID ADN40040 standard; protein; 87 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C410.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 46.5%; Score 214.5; DB 7; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 688
ID ADI36718 standard; protein; 87 AA.
DE Human PLML #2.
PN US2003225014-A1.
PD 04-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 46.5%; Score 214.5; DB 8; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 689
ID ADK70447 standard; protein; 87 AA.
DE Respiratory disease differentially expressed protein #13.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 46.5%; Score 214.5; DB 8; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 690
ID ADQ80368 standard; protein; 87 AA.
DE FXYD domain contaiing ion transport regulator 3 protein.
PN WO2004063709-A2.
PD 29-JUL-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 46.5%; Score 214.5; DB 8; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 691
ID ADZ69596 standard; protein; 87 AA.
DE Human phospholemman-like protein (PLML) SEQ ID NO:10.
PN US2005101558-A1.
PD 12-MAY-2005.
PA (WATT/) WATT A T.
Query Match 46.5%; Score 214.5; DB 9; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 692
ID AEB29726 standard; protein; 87 AA.
DE Human FXYD domain-containing ion transport regulator 3.
PN WO2005067667-A2.
PD 28-JUL-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 46.5%; Score 214.5; DB 9; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 693
ID ABJ19334 standard; protein; 116 AA.
DE NOVX related protein SEQ ID No 34.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 46.5%; Score 214.5; DB 6; Length 116;
Best Local Similarity 54.5%; Pred. No. 1e-18;
RESULT 694
ID ADO41668 standard; protein; 116 AA.
DE Novel human polypeptide NOV13b.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (ZERH/) ZERHUSEN B D.
PA (LILL/) LI L.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (PENA/) PENA C E A.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (LEIT/) LEITE M W.
PA (RAST/) RASTELLI L.
PA (MACD/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GUOX/) GUO X S.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (HJAL/) HJALT T.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (MALY/) MALYANKAR U M.
PA (PADI/) PADIGARU M.
PA (JIWW/) JI W.
PA (SMIT/) SMITHSON G.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Query Match 46.5%; Score 214.5; DB 8; Length 116;
Best Local Similarity 54.5%; Pred. No. 1e-18;
RESULT 695
ID ABJ19333 standard; protein; 86 AA.
DE NOVX related protein SEQ ID No 32.
PN WO200299062-A2.
PD 12-DEC-2002.

PA (CURA-) CURAGEN CORP.
Query Match 45.4%; Score 209.5; DB 6; Length 86;
Best Local Similarity 54.0%; Pred. No. 2.9e-18;
RESULT 696
ID ADO41666 standard; protein; 86 AA.
DE Novel human polypeptide NOV13a.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (ZERH/) ZERHUSEN B D.
PA (LILL/) LI L.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (PENA/) PENA C E A.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (LEIT/) LEITE M W.
PA (RAST/) RASTELLI L.
PA (MACD/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GUOX/) GUO X S.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (HJAL/) HJALT T.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (MALY/) MALYANKAR U M.
PA (PADI/) PADIGARU M.
PA (JIWW/) JI W.
PA (SMIT/) SMITHSON G.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Query Match 45.4%; Score 209.5; DB 8; Length 86;
Best Local Similarity 54.0%; Pred. No. 2.9e-18;
RESULT 697
ID ABR47468 standard; protein; 113 AA.
DE Breast cancer associated protein sequence SEQ ID NO:168.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 41.5%; Score 191.5; DB 6; Length 113;
Best Local Similarity 42.1%; Pred. No. 8e-16;
RESULT 698
ID ADB75318 standard; protein; 113 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.5%; Score 191.5; DB 7; Length 113;
Best Local Similarity 42.1%; Pred. No. 8e-16;
RESULT 699
ID ADN40039 standard; protein; 113 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C409.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 41.5%; Score 191.5; DB 7; Length 113;
Best Local Similarity 42.1%; Pred. No. 8e-16;
RESULT 700
ID AAB53415 standard; protein; 150 AA.
DE Human colon cancer antigen protein sequence SEQ ID NO:955.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.5%; Score 191.5; DB 3; Length 150;
Best Local Similarity 42.1%; Pred. No. 1.2e-15;
RESULT 701
ID ADI36717 standard; protein; 111 AA.
DE Human PLML #1.
PN US2003225014-A1.
PD 04-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 38.1%; Score 175.5; DB 8; Length 111;
Best Local Similarity 41.2%; Pred. No. 8.3e-14;
RESULT 702
ID ADZ69595 standard; protein; 111 AA.
DE Human phospholemman-like protein (PLML) SEQ ID NO:3.
PN US2005101558-A1.
PD 12-MAY-2005.
PA (WATT/) WATT A T.
Query Match 38.1%; Score 175.5; DB 9; Length 111;
Best Local Similarity 41.2%; Pred. No. 8.3e-14;
RESULT 703
ID ABG75841 standard; protein; 67 AA.
DE Transporters and ion channels protein 23, TRICH-23.
PN WO2003016493-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 32.5%; Score 150; DB 6; Length 67;
Best Local Similarity 56.6%; Pred. No. 7.4e-11;
RESULT 704
ID ABU52799 standard; protein; 83 AA.
DE Human signal transduction-associated DKFZphfbr2_82i17 homologue.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 28.0%; Score 129; DB 4; Length 83;
Best Local Similarity 41.3%; Pred. No. 4.5e-08;
RESULT 705
ID AAW75161 standard; protein; 92 AA.
DE Human secreted protein encoded by gene 50 clone HHSDZ57.
PN WO9839446-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.0%; Score 129; DB 2; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 706
ID AAY24749 standard; protein; 92 AA.
DE Human phospholemman homologue protein.
PN US5919655-A.
PD 06-JUL-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 28.0%; Score 129; DB 2; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 707
ID AAY59689 standard; protein; 92 AA.
DE Secreted protein 26-44-1-B5-CL3_1.
PN WO9940189-A2.
PD 12-AUG-1999.
PA (GEST) GENSET.
Query Match 28.0%; Score 129; DB 2; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 708
ID AAY48331 standard; protein; 92 AA.
DE Human prostate cancer-associated protein 28.
PN DE19811194-A1.
PD 16-SEP-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 28.0%; Score 129; DB 2; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 709
ID AAW92960 standard; protein; 92 AA.
DE Human PLM protein.
PN WO9905276-A1.
PD 04-FEB-1999.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 28.0%; Score 129; DB 2; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 710
ID ABB97244 standard; protein; 92 AA.
DE Novel human protein SEQ ID NO: 512.

PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 28.0%; Score 129; DB 5; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 711
ID ABO02037 standard; protein; 92 AA.
DE Novel human secreted protein #105.
PN US2003027132-A1.
PD 06-FEB-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (FISC/) FISCHER C L.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D R.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (SHIY/) SHI Y.
Query Match 28.0%; Score 129; DB 6; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 712
ID ADE58521 standard; protein; 92 AA.
DE Human Protein O00168, SEQ ID NO 4396.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 28.0%; Score 129; DB 7; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 713
ID ADE58525 standard; protein; 92 AA.
DE Human Protein O00168, SEQ ID NO 4400.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 28.0%; Score 129; DB 7; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 714
ID ADE83505 standard; protein; 92 AA.
DE Human Protein O00168, SEQ ID NO 11101.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 28.0%; Score 129; DB 7; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 715
ID ADJ69464 standard; protein; 92 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1270.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 28.0%; Score 129; DB 7; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 716
ID ADM77839 standard; protein; 92 AA.
DE Human protein #36.
PN US2003162176-A1.
PD 28-AUG-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 28.0%; Score 129; DB 7; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 717
ID ADN05844 standard; protein; 92 AA.
DE Antipsoriatic protein sequence #1085.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.0%; Score 129; DB 8; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 718
ID ADP19520 standard; protein; 92 AA.
DE Human secreted polypeptide #371.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 28.0%; Score 129; DB 8; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 719
ID ADZ12438 standard; protein; 92 AA.
DE Human secreted protein sequence encoded by gene 50 SEQ ID NO:238.
PN US6878687-B1.
PD 12-APR-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.0%; Score 129; DB 9; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 720
ID ADZ89299 standard; protein; 92 AA.
DE Secreted protein encoded by extended EST cDNA #36.
PN US2005106599-A1.
PD 19-MAY-2005.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 28.0%; Score 129; DB 9; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.1e-08;
RESULT 721
ID AAW75106 standard; protein; 93 AA.
DE Human secreted protein encoded by gene 50 clone HHSDZ57.
PN WO9839446-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.0%; Score 129; DB 2; Length 93;
Best Local Similarity 41.3%; Pred. No. 5.2e-08;
RESULT 722
ID ABO01982 standard; protein; 93 AA.
DE Novel human secreted protein #50.
PN US2003027132-A1.
PD 06-FEB-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (FISC/) FISCHER C L.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D R.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (SHIY/) SHI Y.
Query Match 28.0%; Score 129; DB 6; Length 93;

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  Best Local Similarity   41.3%;  Pred. No. 5.2e-08;
RESULT 723
ID   ADZ12383 standard; protein; 93 AA.
DE   Human secreted protein sequence encoded by gene 50 SEQ ID NO:183.
PN   US6878687-B1.
PD   12-APR-2005.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             28.0%;  Score 129;  DB 9;  Length 93;
  Best Local Similarity   41.3%;  Pred. No. 5.2e-08;
RESULT 724
ID   ABO02067 standard; protein; 70 AA.
DE   Novel human secreted protein associated protein fragment #12.
PN   US2003027132-A1.
PD   06-FEB-2003.
PA   (RUBE/) RUBEN S M.
PA   (ROSE/) ROSEN C A.
PA   (FISC/) FISCHER C L.
PA   (SOPP/) SOPPET D R.
PA   (CART/) CARTER K C.
PA   (BEDN/) BEDNARIK D R.
PA   (ENDR/) ENDRESS G A.
PA   (YUGG/) YU G.
PA   (NIJJ/) NI J.
PA   (FENG/) FENG P.
PA   (YOUN/) YOUNG P E.
PA   (GREE/) GREENE J M.
PA   (FERR/) FERRIE A M.
PA   (DUAN/) DUAN R.
PA   (HUJJ/) HU J.
PA   (FLOR/) FLORENCE K A.
PA   (OLSE/) OLSEN H S.
PA   (EBNE/) EBNER R.
PA   (BREW/) BREWER L A.
PA   (SHIY/) SHI Y.
  Query Match             26.2%;  Score 121;  DB 6;  Length 70;
  Best Local Similarity   44.9%;  Pred. No. 3.7e-07;
RESULT 725
ID   ADZ12469 standard; protein; 70 AA.
DE   Human gene 50 secreted protein related sequence SEQ ID NO:269.
PN   US6878687-B1.
PD   12-APR-2005.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             26.2%;  Score 121;  DB 9;  Length 70;
  Best Local Similarity   44.9%;  Pred. No. 3.7e-07;
RESULT 726
ID   AAY12377 standard; protein; 63 AA.
DE   Human 5' EST secreted protein SEQ ID NO:408.
PN   WO9906548-A2.
PD   11-FEB-1999.
PA   (GEST ) GENSET.
  Query Match             24.7%;  Score 114;  DB 2;  Length 63;
  Best Local Similarity   43.1%;  Pred. No. 2.5e-06;
RESULT 727
ID   ADE58523 standard; protein; 92 AA.
DE   Rat Protein O08589, SEQ ID NO 4398.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
  Query Match             24.7%;  Score 114;  DB 7;  Length 92;
  Best Local Similarity   31.6%;  Pred. No. 4.1e-06;
RESULT 728
ID   ADE58519 standard; protein; 92 AA.
DE   Rat Protein O08589, SEQ ID NO 4394.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
  Query Match             24.7%;  Score 114;  DB 7;  Length 92;
  Best Local Similarity   31.6%;  Pred. No. 4.1e-06;
RESULT 729
ID   ADE83503 standard; protein; 92 AA.
DE   Rat Protein O08589, SEQ ID NO 11099.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
  Query Match             24.7%;  Score 114;  DB 7;  Length 92;
  Best Local Similarity   31.6%;  Pred. No. 4.1e-06;
RESULT 730
ID   AAM38777 standard; protein; 138 AA.
DE   Human polypeptide SEQ ID NO 1922.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             24.6%;  Score 113.5;  DB 4;  Length 138;
  Best Local Similarity   34.2%;  Pred. No. 8e-06;
RESULT 731
ID   AAU14339 standard; protein; 138 AA.
DE   Human novel protein #210.
PN   WO200155437-A2.
PD   02-AUG-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             24.6%;  Score 113.5;  DB 4;  Length 138;
  Best Local Similarity   34.2%;  Pred. No. 8e-06;
RESULT 732
ID   AAM40563 standard; protein; 155 AA.
DE   Human polypeptide SEQ ID NO 5494.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             24.6%;  Score 113.5;  DB 4;  Length 155;
  Best Local Similarity   34.2%;  Pred. No. 9.3e-06;
RESULT 733
ID   AAW51104 standard; protein; 95 AA.
DE   A human phospholemman-like protein.
PN   WO9814572-A1.
PD   09-APR-1998.
PA   (INCY-) INCYTE PHARM INC.
  Query Match             24.4%;  Score 112.5;  DB 2;  Length 95;
  Best Local Similarity   36.0%;  Pred. No. 6.6e-06;
RESULT 734
ID   AAU14575 standard; protein; 95 AA.
DE   Human novel protein #446.
PN   WO200155437-A2.
PD   02-AUG-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             24.4%;  Score 112.5;  DB 4;  Length 95;
  Best Local Similarity   36.0%;  Pred. No. 6.6e-06;
RESULT 735
ID   ABU52798 standard; protein; 95 AA.
DE   Human signal transduction-associated protein from DKFZphfbr2_82i17.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
  Query Match             24.4%;  Score 112.5;  DB 4;  Length 95;
  Best Local Similarity   36.0%;  Pred. No. 6.6e-06;
RESULT 736
ID   ADH80893 standard; protein; 95 AA.
DE   Human polypeptide #210.
PN   US2003232054-A1.
PD   18-DEC-2003.
PA   (TANG/) TANG Y T.
PA   (LIUC/) LIU C.
PA   (ASUN/) ASUNDI V.
PA   (CHEN/) CHEN R.
PA   (QIAN/) QIAN X B.
PA   (WANG/) WANG Z W.
PA   (WEHR/) WEHRMAN T.
PA   (ZHAN/) ZHANG J.
PA   (ZHOU/) ZHOU P.
PA   (CAOY/) CAO Y.
PA   (DRMA/) DRMANAC R T.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 95;
  Best Local Similarity   36.0%;  Pred. No. 6.6e-06;
RESULT 737
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ID ABM81305 standard; protein; 95 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82051, SEQ:3370.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 95;
Best Local Similarity 36.0%; Pred. No. 6.6e-06;
RESULT 738
ID AAW74882 standard; protein; 96 AA.
DE Human secreted protein encoded by gene 154 clone HE6FL83.
PN WO9839448-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 24.4%; Score 112.5; DB 2; Length 96;
Best Local Similarity 36.0%; Pred. No. 6.7e-06;
RESULT 739
ID ABG95333 standard; protein; 96 AA.
DE Human novel secreted protein #154.
PN US6420526-B1.
PD 16-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 24.4%; Score 112.5; DB 5; Length 96;
Best Local Similarity 36.0%; Pred. No. 6.7e-06;
RESULT 740
ID ABO34527 standard; protein; 96 AA.
DE Region of human secreted protein encoded by cDNA sequence #154.
PN US2003049618-A1.
PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 24.4%; Score 112.5; DB 6; Length 96;
Best Local Similarity 36.0%; Pred. No. 6.7e-06;
RESULT 741
ID ADI23188 standard; protein; 96 AA.
DE Novel human secreted protein seq id 473.
PN US2003175858-A1.
PD 18-SEP-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 24.4%; Score 112.5; DB 7; Length 96;
Best Local Similarity 36.0%; Pred. No. 6.7e-06;
RESULT 742
ID ADH74190 standard; protein; 96 AA.
DE Human secreted protein #154.
PN US2003225248-A1.
PD 04-DEC-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 24.4%; Score 112.5; DB 8; Length 96;
Best Local Similarity 36.0%; Pred. No. 6.7e-06;
RESULT 743
ID AAY66680 standard; protein; 120 AA.
DE Membrane-bound protein PRO1056.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 3; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 744
ID AAU12388 standard; protein; 120 AA.
DE Human PRO1056 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 4; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 745
ID AAB65203 standard; protein; 120 AA.
DE Human PRO1056 (UNQ521) protein sequence SEQ ID NO:199.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 4; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 746
ID ABU58018 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 747
ID ABU59096 standard; protein; 120 AA.
DE Novel human secreted or transmembrane protein PRO1056.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 748
ID ABU82608 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 749
ID ABO17832 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003032156-A1.
PD 13-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 750
ID ABU60527 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, #77.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 751
ID ABU13909 standard; protein; 120 AA.
DE Human PRO1056 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 752
ID ABU81086 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 753
ID ABU72494 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 754
ID ABU66786 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 755
ID ABU59867 standard; protein; 120 AA.
DE Novel secreted and transmembrane protein PRO1056.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 756
ID ABU59243 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, #77.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 757
ID ABO25940 standard; protein; 120 AA.
DE Human PRO1056 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 758
ID ABO25057 standard; protein; 120 AA.
DE Human secreted/transmembrane protein (PRO) #217.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 759
ID ABU58949 standard; protein; 120 AA.
DE Human sectreted/transmembrane protein, #77.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 760
ID ABU92327 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 761
ID ABU59392 standard; protein; 120 AA.
DE Novel human secreted or transmembrane protein PRO826.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 762
ID ABU67062 standard; protein; 120 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 434.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 763
ID ABU92158 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 764
ID ABU10864 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 765
ID ABU81616 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 766
ID ABU88555 standard; protein; 120 AA.
DE Human secreted and transmembrane polypeptide PRO1056.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 767
ID ABO34069 standard; protein; 120 AA.
DE Human PRO1056 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 768
ID ADA45953 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003022328-A1.

PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 769
ID ADA76384 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 770
ID ADA19034 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 771
ID ADA61657 standard; protein; 120 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 772
ID ADB19442 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 773
ID ADB27983 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 774
ID ADA86462 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 775
ID ADB16026 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 776
ID ADA37710 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 777
ID ADA47812 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 778
ID ADA21396 standard; protein; 120 AA.
DE Human secreted/transmembrane polypeptide PRO1056.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 779
ID ADA10183 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, PRO1056.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 780
ID ADA67607 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 781
ID ADB30614 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 782
ID ADA85910 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 783
ID ADA17727 standard; protein; 120 AA.
DE Human PRO1056 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 784
ID ADA97122 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 785
ID ADA79426 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 786
ID ADA87565 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 787

ID ADB16767 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 788
ID ADA27835 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 789
ID ADA91859 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 790
ID ADB14922 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 791
ID ADB18883 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 792
ID ADA94098 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 793
ID ADB19994 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 794
ID ADB13306 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 795
ID ABO43365 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 796
ID ADA94415 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 797
ID ADA74560 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 798
ID ADB24793 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 799
ID ADA82317 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 800
ID ADA75280 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 801
ID ADA85358 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 802
ID ADA84806 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 803
ID ADB30062 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 804
ID ADA80590 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 805
ID ADA75832 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082703-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 806
ID ADA38640 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 807
ID ADA47057 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 808
ID ADB25353 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 809
ID ADA93529 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 810
ID ADB26879 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 811
ID ADB31166 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 812
ID ADA92761 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 813
ID ADA61094 standard; protein; 120 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 814
ID ADB24241 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 815
ID ADA96570 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 816
ID ADA81142 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 817
ID ADA96018 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 818
ID ADB26327 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 819
ID ADB21812 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 820
ID ADA77591 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 821
ID ADB18331 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 822
ID ADA87014 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 823
ID ADA88117 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 824

ID ADA46505 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 825
ID ADB28535 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 826
ID ADB29087 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 827
ID ABO53155 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 828
ID ADA77039 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 829
ID ADA22322 standard; protein; 120 AA.
DE Human secreted/transmembrane polypeptide PRO1056.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 830
ID ADA88669 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 831
ID ADA97674 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 832
ID ADB27431 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 833
ID ADB22364 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 834
ID ABO22525 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 835
ID ADA06488 standard; protein; 120 AA.
DE Human secreted/transmembrane PRO polypeptide #50.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 836
ID ADA39181 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 837
ID ADA67055 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 838
ID ADB22916 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 839
ID ADB23689 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 840
ID ADA92411 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 841
ID ADB15474 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 842
ID ADB38726 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 843
ID ADB96207 standard; protein; 120 AA.

DE Human PRO polypeptide #50.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 844
ID ADB38174 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 845
ID ADB66646 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 846
ID ADB89726 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 847
ID ADB90458 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 848
ID ADB39559 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 849
ID ADB47182 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 850
ID ADB86789 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 851
ID ADB77394 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 852
ID ADB34551 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 853
ID ADB35655 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 854
ID ADB33999 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 855
ID ADB35103 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 856
ID ADB36207 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 857
ID ADB46602 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 858
ID ADC57679 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 859
ID ADC55043 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 860
ID ADC11910 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 861
ID ADC56332 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 862

ID ADC07387 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 863
ID ADC11377 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 864
ID ADC50475 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 865
ID ADC72022 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 866
ID ADC60001 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 867
ID ADC53008 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 868
ID ADC57362 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 869
ID ADC60553 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 870
ID ADC51028 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 871
ID ADC65555 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 872
ID ADC54653 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 873
ID ADC53614 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 874
ID ADC59137 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 875
ID ADC56015 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 876
ID ADC58585 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 877
ID ADC14499 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 878
ID ADD08031 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 879
ID ADD03259 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 880
ID ADC90251 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;

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  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 881
ID   ADC81856 standard; protein; 120 AA.
DE   Human PRO polypeptide #50.
PN   US2003083461-A1.
PD   01-MAY-2003.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 882
ID   ADC69670 standard; protein; 120 AA.
DE   Human PRO polypeptide #217.
PN   US2003194770-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 883
ID   ADC48559 standard; protein; 120 AA.
DE   Human PRO polypeptide #217.
PN   US2003194773-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 884
ID   ADD10088 standard; protein; 120 AA.
DE   Human PRO polypeptide #217.
PN   US2003194776-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 885
ID   ADD07498 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2002193299-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 886
ID   ADD04663 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003087354-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 887
ID   ADC82389 standard; protein; 120 AA.
DE   Human PRO polypeptide #50.
PN   US2003059833-A1.
PD   27-MAR-2003.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 888
ID   ADC80619 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003092103-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 889
ID   ADD11126 standard; protein; 120 AA.
DE   Human PRO polypeptide #217.
PN   US2003194774-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 890
ID   ADC48007 standard; protein; 120 AA.
DE   Human PRO polypeptide #217.
PN   US2003194771-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 891
ID   ADD08569 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003073090-A1.
PD   17-APR-2003.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 892
ID   ADC80067 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003087358-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 893
ID   ADD06818 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2002193300-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 894
ID   ADD09536 standard; protein; 120 AA.
DE   Human PRO polypeptide #217.
PN   US2003194775-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 895
ID   ADC83065 standard; protein; 120 AA.
DE   Human PRO polypeptide #50.
PN   US2003059783-A1.
PD   27-MAR-2003.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 896
ID   ADD41249 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003203438-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 897
ID   ADD52388 standard; protein; 120 AA.
DE   Human PRO polypeptide #217.
PN   US2003194769-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 898
ID   ADD53128 standard; protein; 120 AA.
DE   Human PRO polypeptide #217.
PN   US2003194792-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 7;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 899
ID   ADD53680 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003203437-A1.
PD   30-OCT-2003.
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PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 900
ID ADD55172 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 901
ID ADD56130 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 902
ID ADD51836 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 903
ID ADD02635 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 904
ID ADD02069 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 905
ID ADD54251 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 906
ID ADD54568 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 907
ID ADD92568 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 908
ID ADD91464 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 909
ID ADE04078 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 910
ID ADE26722 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 911
ID ADE32375 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 912
ID ADE22307 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 913
ID ADD79531 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 914
ID ADE42067 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 915
ID ADE17884 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 916
ID ADD92016 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 917
ID ADE33479 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 918
ID ADE34031 standard; protein; 120 AA.

DE Novel human secreted and transmembrane protein PRO1056.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 919
ID ADD80083 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 920
ID ADD93120 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 921
ID ADE19540 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 922
ID ADE18988 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 923
ID ADE43184 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 924
ID ADD95973 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 925
ID ADE22859 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 926
ID ADD78977 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 927
ID ADE26189 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 928
ID ADE32927 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 929
ID ADE42619 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 930
ID ADD80635 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 931
ID ADD89663 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 932
ID ADE40947 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 933
ID ADE04746 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 934
ID ADE92875 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 935
ID ADF67126 standard; protein; 120 AA.
DE Human PRO1056 amino acid sequence SEQ ID NO:199.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 936
ID ADG21584 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207355-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 937
ID ADG23225 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 938
ID ADF97560 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 939
ID ADG80624 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 940
ID ADG80072 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 941
ID ADH55364 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 942
ID ADH55916 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 943
ID ADI35380 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 944
ID ADI64135 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 945
ID ADI65084 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 946
ID ADI63583 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 947
ID ADH81997 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 948
ID ADH99872 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 949
ID ADH81445 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 950
ID ADM82614 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 951
ID ADN16013 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 952
ID ADN16642 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 953
ID ADN15461 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 954
ID ADN14909 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 955

ID ADC81171 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 956
ID ADD76619 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 957
ID ADD87983 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 958
ID ADD86387 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 959
ID ADE75835 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 960
ID ADE23411 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 961
ID ADE23963 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 962
ID ADE24606 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 963
ID ADD87431 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 964
ID ADE89297 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 965
ID ADE18436 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 966
ID ADE88745 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 967
ID ADE94765 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 968
ID ADE91176 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 969
ID ADF35325 standard; protein; 120 AA.
DE Human PRO1056 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 970
ID ADE95317 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 971
ID ADE93427 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 972
ID ADF35008 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 973
ID ADE92323 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003199051-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 974
ID ADE90624 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 975
ID ADE91771 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 976
ID ADG11575 standard; protein; 120 AA.
DE Human PRO1056 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 977
ID ADG02350 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 978
ID ADG22136 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 979
ID ADG20206 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 980
ID ADF98112 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 981
ID ADG24329 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 982
ID ADF98683 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 983
ID ADG03514 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 984
ID ADF99235 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 985
ID ADG16820 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 986
ID ADG05279 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 987
ID ADG19546 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 988
ID ADG13383 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 989
ID ADG08440 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 990
ID ADG15610 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 991
ID ADF97008 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

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  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 992
ID   ADG06193 standard; protein; 120 AA.
DE   Human PRO polypeptide #217.
PN   US2003207374-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 993
ID   ADG23777 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003207389-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 994
ID   ADG04066 standard; protein; 120 AA.
DE   Human PRO polypeptide #217.
PN   US2003207423-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 995
ID   ADG24967 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003207427-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 996
ID   ADG07264 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003207350-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 997
ID   ADG07816 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003207356-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 998
ID   ADG55311 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003194778-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 999
ID   ADG60975 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003207390-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 1000
ID   ADG62079 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003207428-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 1001
ID   ADG82280 standard; protein; 120 AA.
DE   Human PRO polypeptide #217.
PN   US2003207358-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 1002
ID   ADG57519 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003207362-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 1003
ID   ADG56967 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003207364-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 1004
ID   ADG55863 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003207365-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 1005
ID   ADG58623 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003207368-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 1006
ID   ADG70989 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003207420-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 1007
ID   ADG58071 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003207363-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 1008
ID   ADG53655 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003207415-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
RESULT 1009
ID   ADG71541 standard; protein; 120 AA.
DE   Novel human secreted and transmembrane protein PRO1056.
PN   US2003207421-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             24.4%;  Score 112.5;  DB 8;  Length 120;
  Best Local Similarity   36.0%;  Pred. No. 9e-06;
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RESULT 1010
ID ADG81728 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1011
ID ADH19445 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1012
ID ADH30690 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1013
ID ADH12057 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1014
ID ADG52479 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1015
ID ADG54207 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1016
ID ADG81176 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1017
ID ADG56415 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1018
ID ADH12681 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1019
ID ADH20938 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1020
ID ADG61527 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1021
ID ADH19978 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1022
ID ADH28614 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1023
ID ADG54759 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1024
ID ADG59799 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1025
ID ADI81223 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1026
ID ADG09966 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1027
ID ADI15437 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1028
ID ADG09314 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2004009547-A1.

PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1029
ID ADI14769 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1030
ID ADI18364 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1031
ID ADJ63645 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1032
ID ADJ77540 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1033
ID ADJ65662 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1034
ID ADM27798 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1035
ID ADM42522 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1036
ID ADM28384 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1037
ID ADI95866 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1038
ID ADI96418 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1039
ID ADS32370 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1040
ID ADT03354 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1041
ID ADZ03405 standard; protein; 120 AA.
DE Human secreted/transmembrane PRO1056 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 9; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1042
ID AEA38462 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, #118.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 9; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1043
ID AEB14151 standard; protein; 120 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 434.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 24.4%; Score 112.5; DB 9; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1044
ID ABB80585 standard; protein; 95 AA.
DE Human sbg1015258PLM protein.
PN WO200222802-A1.
PD 21-MAR-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 24.3%; Score 112; DB 5; Length 95;
Best Local Similarity 35.9%; Pred. No. 7.7e-06;
RESULT 1045
ID AAW75005 standard; protein; 69 AA.
DE Human secreted protein encoded by gene 154 clone HE6FL83.
PN WO9839448-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.0%; Score 106; DB 2; Length 69;
Best Local Similarity 40.0%; Pred. No. 2.9e-05;
RESULT 1046
ID ABG95466 standard; protein; 69 AA.
DE Human novel secreted protein #287.
PN US6420526-B1.
PD 16-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.0%; Score 106; DB 5; Length 69;
Best Local Similarity 40.0%; Pred. No. 2.9e-05;
RESULT 1047
ID ABO34660 standard; protein; 69 AA.
DE Region of human secreted protein encoded by cDNA sequence #287.
PN US2003049618-A1.
PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 23.0%; Score 106; DB 6; Length 69;
Best Local Similarity 40.0%; Pred. No. 2.9e-05;
RESULT 1048
ID ADI23321 standard; protein; 69 AA.
DE Novel human secreted protein seq id 606.
PN US2003175858-A1.
PD 18-SEP-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 23.0%; Score 106; DB 7; Length 69;
Best Local Similarity 40.0%; Pred. No. 2.9e-05;
RESULT 1049
ID ADH74323 standard; protein; 69 AA.
DE Human secreted protein #287.
PN US2003225248-A1.
PD 04-DEC-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.0%; Score 106; DB 8; Length 69;
Best Local Similarity 40.0%; Pred. No. 2.9e-05;
RESULT 1050
ID ABG26346 standard; protein; 110 AA.
DE Novel human diagnostic protein #26337.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.9%; Score 105.5; DB 4; Length 110;
Best Local Similarity 33.8%; Pred. No. 6.2e-05;
RESULT 1051
ID AAY13121 standard; protein; 72 AA.
DE Human secreted protein encoded by 5' EST SEQ ID NO: 135.
PN WO9906552-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 21.6%; Score 99.5; DB 2; Length 72;
Best Local Similarity 36.4%; Pred. No. 0.00021;
RESULT 1052
ID ABP03457 standard; protein; 63 AA.
DE Human ORFX protein sequence SEQ ID NO:6896.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 20.8%; Score 96; DB 5; Length 63;
Best Local Similarity 32.8%; Pred. No. 0.00048;
RESULT 1053
ID ABG75825 standard; protein; 80 AA.
DE Transporters and ion channels protein 7, TRICH-7.
PN WO2003016493-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 20.6%; Score 95; DB 6; Length 80;
Best Local Similarity 31.3%; Pred. No. 0.00088;
RESULT 1054
ID ABM85184 standard; protein; 148 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5433.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 20.6%; Score 95; DB 8; Length 148;
Best Local Similarity 36.5%; Pred. No. 0.0019;
RESULT 1055
ID ABR82718 standard; protein; 115 AA.
DE Human IWU-1 protein.
PN WO2003064603-A2.
PD 07-AUG-2003.
PA (UYRP) UNIV ROCHESTER.
Query Match 20.4%; Score 94; DB 7; Length 115;
Best Local Similarity 43.9%; Pred. No. 0.0019;
RESULT 1056
ID ABM85185 standard; protein; 147 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5434.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.

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  Query Match             20.4%;  Score 94;  DB 8;  Length 147;
  Best Local Similarity   43.9%;  Pred. No. 0.0026;
RESULT 1057
ID   AAY13945 standard; protein; 178 AA.
DE   Human transmembrane protein, HP10479.
PN   WO9918203-A2.
PD   15-APR-1999.
PA   (SAGA ) SAGAMI CHEM RES CENT.
PA   (PROT-) PROTEGENE INC.
  Query Match             20.4%;  Score 94;  DB 2;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1058
ID   AAY41674 standard; protein; 178 AA.
DE   Human channel-related molecule HCRM-2.
PN   WO9943807-A2.
PD   02-SEP-1999.
PA   (INCY-) INCYTE PHARM INC.
  Query Match             20.4%;  Score 94;  DB 2;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1059
ID   AAU29294 standard; protein; 178 AA.
DE   Human PRO polypeptide sequence #271.
PN   WO200168848-A2.
PD   20-SEP-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 4;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1060
ID   AAM38819 standard; protein; 178 AA.
DE   Human polypeptide SEQ ID NO 1964.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             20.4%;  Score 94;  DB 4;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1061
ID   ABB90357 standard; protein; 178 AA.
DE   Human polypeptide SEQ ID NO 2733.
PN   WO200190304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             20.4%;  Score 94;  DB 5;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1062
ID   AAO17172 standard; protein; 178 AA.
DE   Human secreted protein SEQ ID NO: 71.
PN   WO200228877-A1.
PD   11-APR-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             20.4%;  Score 94;  DB 5;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1063
ID   ABG64783 standard; protein; 178 AA.
DE   Human albumin fusion protein #1458.
PN   WO200177137-A1.
PD   18-OCT-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             20.4%;  Score 94;  DB 5;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1064
ID   ABU58670 standard; protein; 178 AA.
DE   Human PRO polypeptide #271.
PN   US2003027272-A1.
PD   06-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1065
ID   ABU88218 standard; protein; 178 AA.
DE   Novel human secreted and transmembrane protein PRO6241.
PN   US2003032127-A1.
PD   13-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1066
ID   ABU84533 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003032112-A1.
PD   13-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1067
ID   ABR66407 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003027278-A1.
PD   06-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1068
ID   ABR65797 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003036159-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1069
ID   ABU99737 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003040070-A1.
PD   27-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1070
ID   ABU82976 standard; protein; 178 AA.
DE   Human PRO polypeptide #271.
PN   US2003032113-A1.
PD   13-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1071
ID   ABU90097 standard; protein; 178 AA.
DE   Novel human secreted and transmembrane protein PRO6241.
PN   US2003036147-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1072
ID   ABR68346 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003027264-A1.
PD   06-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1073
ID   ABU96399 standard; protein; 178 AA.
DE   Novel human secreted and transmembrane protein PRO6241.
PN   US2003036144-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1074
ID   ABU92830 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003036149-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1075
ID   ABO08907 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003044923-A1.
PD   06-MAR-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1076
ID   ABO02959 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
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PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1077
ID ABR75113 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1078
ID ABR94875 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1079
ID ABU85848 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1080
ID ABU99008 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1081
ID ABU98223 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1082
ID ABU91929 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1083
ID ABU89622 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1084
ID ABU86463 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1085
ID ABU67676 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1086
ID ABU80704 standard; protein; 178 AA.
DE Human PRO protein #271.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1087
ID ABR99622 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1088
ID ABR99012 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1089
ID ABO16535 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1090
ID ABR92435 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1091
ID ABO19076 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1092
ID ABR78497 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1093
ID ABU85233 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1094
ID ABO00372 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1095
ID ABO11704 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1096
ID ABO02349 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003040054-A1.

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PD   27-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1097
ID   ADA41202 standard; protein; 178 AA.
DE   Human secreted protein.
PN   WO2002102993-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1098
ID   ABU88923 standard; protein; 178 AA.
DE   Novel human secreted and transmembrane protein PRO6241.
PN   US2003036133-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1099
ID   ABU83618 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003036134-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1100
ID   ABO06419 standard; protein; 178 AA.
DE   Novel human secreted and transmembrane protein PRO6241.
PN   US2003022294-A1.
PD   30-JAN-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1101
ID   ABR59455 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003027275-A1.
PD   06-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1102
ID   ABO09517 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003027324-A1.
PD   06-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1103
ID   ABO19381 standard; protein; 178 AA.
DE   Novel human secreted and transmembrane protein PRO6241.
PN   US2003036118-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1104
ID   ABO11399 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003036123-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1105
ID   ABR67017 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003036148-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1106
ID   ABO16230 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003040060-A1.
PD   27-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1107
ID   ABO13936 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003044916-A1.
PD   06-MAR-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1108
ID   ABU65839 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein, SEQ ID 542.
PN   US2003036156-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1109
ID   ABO07687 standard; protein; 178 AA.
DE   Human PRO polypeptide #271.
PN   US2003032117-A1.
PD   13-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1110
ID   ABO03874 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003036128-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1111
ID   ABR67322 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003027266-A1.
PD   06-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1112
ID   ABO15925 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003054483-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1113
ID   ABU56206 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein, PRO6241.
PN   US2003022298-A1.
PD   30-JAN-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1114
ID   ABU65534 standard; protein; 178 AA.
DE   Human PRO polypeptide #271.
PN   US2003032102-A1.
PD   13-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1115
ID   ABU95479 standard; protein; 178 AA.
DE   Novel human secreted and transmembrane protein PRO6241.
PN   US2003036117-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1116
ID   ABU71382 standard; protein; 178 AA.
DE   Human PRO6241 protein.
PN   US2003036143-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 6;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
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RESULT 1117
ID ABO07992 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1118
ID ABR70233 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1119
ID ABR69566 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1120
ID ABO01707 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1121
ID ABU81509 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1122
ID ABR60306 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1123
ID ABR68041 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1124
ID ABR65429 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1125
ID ABR68651 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1126
ID ABR72063 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1127
ID ABU85543 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1128
ID ABU89233 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1129
ID ABU83313 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1130
ID ABU95169 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1131
ID ABU90717 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1132
ID ABU84228 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1133
ID ABU93879 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1134
ID ABR65124 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1135
ID ABR68956 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1136
ID ABO06772 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1137
ID ABR99317 standard; protein; 178 AA.

DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1138
ID ABU57201 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1139
ID ABU86153 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1140
ID ABU82440 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1141
ID ABU87451 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1142
ID ABU83923 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1143
ID ABO08297 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1144
ID ABU82008 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1145
ID ABU66172 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1146
ID ABR60001 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1147
ID ABU94189 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1148
ID ABO00062 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1149
ID ABR66712 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1150
ID ABR91130 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1151
ID ABU94557 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1152
ID ABU79439 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1153
ID ABU86768 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1154
ID ABU87073 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1155
ID ABU94862 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1156
ID ABO04789 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1157
ID ABR70538 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1158
ID ABU98703 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1159
ID ABR66102 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1160
ID ABR64819 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1161
ID ABU79744 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1162
ID ABU93135 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1163
ID ABU96094 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1164
ID ABU91314 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1165
ID ABU90407 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1166
ID ABO09822 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1167
ID ABO11094 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1168
ID ABR71148 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1169
ID ABU87756 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1170
ID ABU91624 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1171
ID ABU84838 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1172
ID ABR69928 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1173
ID ABU80305 standard; protein; 178 AA.
DE Human PRO protein #271.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1174
ID ABU93574 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1175
ID ABO10127 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1176
ID ABO09212 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1177
ID ABU10780 standard; protein; 178 AA.
DE Human secreted/transmembrane protein #271.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1178
ID ABU95789 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032115-A1.

PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1179
ID ABU96998 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1180
ID ABR70843 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1181
ID ABO05194 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1182
ID ABO08602 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1183
ID ABO05809 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1184
ID ABR74198 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1185
ID ABR95790 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1186
ID ABR81087 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1187
ID ABR81392 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1188
ID ABM01088 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1189
ID ABR88690 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1190
ID ABM77511 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1191
ID ABO28995 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1192
ID ABO31740 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1193
ID ABM08157 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1194
ID ABO40637 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1195
ID ABO36062 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1196
ID ABO44201 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1197
ID ADA78294 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.

PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1198
ID ABM24996 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1199
ID ABO03264 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1200
ID ABR90520 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1201
ID ABM17434 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1202
ID ABR95180 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1203
ID ABR95485 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1204
ID ABO21723 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1205
ID ABR97987 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1206
ID ABR87775 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1207
ID ABM77816 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1208
ID ABM28046 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1209
ID ABM06327 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1210
ID ABM03833 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1211
ID ABM35284 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1212
ID ABM26521 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1213
ID ABO48303 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1214
ID ABR93045 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1215
ID ABO24806 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1216
ID ABM11817 standard; protein; 178 AA.

DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1217
ID ABM02918 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1218
ID ABM16214 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1219
ID ABO27775 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1220
ID ABM29266 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1221
ID ABM07242 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1222
ID ABM21336 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1223
ID ABM09682 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1224
ID ABO41552 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1225
ID ABO36367 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1226
ID ABO43896 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1227
ID ABM76596 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1228
ID ABM76292 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1229
ID ABM25911 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1230
ID ABM26216 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1231
ID ABO03569 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1232
ID ABO02654 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1233
ID ABR90825 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1234
ID ABR73893 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1235
ID ABO17145 standard; protein; 178 AA.

DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1236
ID ABR94570 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1237
ID ABR76077 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1238
ID ABR71453 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1239
ID ABR93350 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1240
ID ABR93655 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1241
ID ABR88080 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1242
ID ABO28080 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1243
ID ABO30215 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1244
ID ABO33424 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1245
ID ABM05112 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1246
ID ABM09072 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1247
ID ABO36672 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1248
ID ABO35757 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1249
ID ABO39722 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1250
ID ABM10597 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1251
ID ABM12122 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1252
ID ABO52268 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1253
ID ABO52573 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1254
ID ABO23891 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1255
ID ABR97377 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1256
ID ABR87165 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1257
ID ABM11207 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1258
ID ABM28351 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1259
ID ABO32350 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1260
ID ABM15477 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1261
ID ABM06632 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1262
ID ABM04443 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1263
ID ABM22556 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1264
ID ABM07852 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1265
ID ABO40942 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1266
ID ABM35589 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1267
ID ABM33352 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1268
ID ABO52878 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1269
ID ABO50438 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1270
ID ABU99432 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1271
ID ABO04484 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1272
ID ABM18654 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054480-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1273
ID ABR97682 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1274
ID ABR80782 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1275
ID ABM01393 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1276
ID ABR88995 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1277
ID ABM13647 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1278
ID ABM21031 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1279
ID ABO42162 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1280
ID ABO42772 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1281
ID ABM10292 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1282
ID ABO38807 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1283
ID ABM33047 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1284
ID ABM22861 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1285
ID ABM75072 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1286
ID ADA80086 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1287
ID ABR96462 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1288
ID ABM02613 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1289
ID ABR86555 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1290
ID ABR86860 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1291
ID ABM16824 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.

PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1292
ID ABM29876 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1293
ID ABO29300 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1294
ID ABM24081 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1295
ID ABM23471 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1296
ID ABM22251 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1297
ID ABO37892 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1298
ID ABM28656 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1299
ID ABM28961 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1300
ID ABM66605 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1301
ID ABM75987 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1302
ID ABM34267 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1303
ID ABM34572 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1304
ID ABO20503 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1305
ID ABO21418 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1306
ID ABO22333 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1307
ID ABR96767 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1308
ID ABR85945 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1309
ID ABR99927 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1310

ID ABM00783 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1311
ID ABM00478 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1312
ID ABO29910 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1313
ID ABM23776 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1314
ID ABM29571 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1315
ID ABO38502 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1316
ID ABO45802 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1317
ID ABM20726 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1318
ID ADA81813 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1319
ID ABO16840 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1320
ID ABO18466 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1321
ID ABO22893 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1322
ID ABO23198 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1323
ID ABR92740 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1324
ID ABR81697 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1325
ID ABM78121 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1326
ID ABR89910 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1327
ID ABM26826 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1328
ID ABM13952 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1329
ID ABO28690 standard; protein; 178 AA.

DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1330
ID ABO30520 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1331
ID ABM07547 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1332
ID ABM04138 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1333
ID ABO37282 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1334
ID ABO41857 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1335
ID ABO35452 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1336
ID ABM25301 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1337
ID ABO47693 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1338
ID ABO47998 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1339
ID ABO48608 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1340
ID ABO51658 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1341
ID ABO51963 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1342
ID ABO50743 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1343
ID ABR79867 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1344
ID ABM17129 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1345
ID ABO18161 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1346
ID ABO21113 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1347
ID ABR97072 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1348
ID ABM12427 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1349
ID ABM16519 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1350
ID ABM24386 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1351
ID ABM14867 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1352
ID ABM04748 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1353
ID ABM06937 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1354
ID ABM09377 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1355
ID ABO39417 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1356
ID ABM75682 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1357
ID ABM25606 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1358
ID ABM20116 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1359
ID ABO47022 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1360
ID ABO47327 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1361
ID ADA83611 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1362
ID ABR71758 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1363
ID ABR72368 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1364
ID ABR98707 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1365
ID ABO07077 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1366
ID ABR85030 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1367
ID ABR73588 standard; protein; 178 AA.

DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1368
ID ABR76682 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1369
ID ABR73283 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1370
ID ABM18349 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1371
ID ABO20808 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1372
ID ABO25551 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1373
ID ABO25856 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1374
ID ABR94265 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1375
ID ABR80172 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1376
ID ABM11512 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1377
ID ABO33119 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1378
ID ABO30825 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1379
ID ABO31130 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1380
ID ABM27436 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1381
ID ABM30181 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1382
ID ABM05717 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1383
ID ABM15782 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1384
ID ABM08767 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1385
ID ABO42467 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1386
ID ABO38197 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1387
ID ABO46107 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1388
ID ABM66910 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1389
ID ADB20654 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1390
ID ABM19811 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1391
ID ABO49523 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1392
ID ABO49828 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1393
ID ADA78906 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1394
ID ABR88385 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1395
ID ABM27131 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1396
ID ABM03528 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1397
ID ABO40027 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1398
ID ABO50133 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1399
ID ABO51048 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1400
ID ABO05504 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1401
ID ABR74808 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1402
ID ABR77287 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1403
ID ABM18044 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1404
ID ABR96095 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1405
ID ABO22028 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1406
ID ABO20198 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1407
ID ABO24501 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1408
ID ABR86250 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1409
ID ABM10902 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1410
ID ABM76901 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1411
ID ABR89605 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1412
ID ABM12732 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1413
ID ABM06022 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1414
ID ABO35147 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1415
ID ABM03223 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1416
ID ABM19201 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1417
ID ABM19506 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1418
ID ABO46717 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1419
ID ABO49218 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1420
ID ABR69261 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1421
ID ABR89300 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1422
ID ABR72673 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1423
ID ABR74503 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;

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  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1424
ID   ABO18771 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003044921-A1.
PD   06-MAR-2003.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1425
ID   ABR80477 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003049739-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1426
ID   ABM01698 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003059882-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1427
ID   ABM02308 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003059884-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1428
ID   ABR87470 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003068687-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1429
ID   ABM13037 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003073186-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1430
ID   ABM30791 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003064443-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1431
ID   ABM24691 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003064444-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1432
ID   ABO29605 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003068697-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1433
ID   ABO31435 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003068710-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1434
ID   ABM14562 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003068686-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1435
ID   ABM09987 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003073178-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1436
ID   ABO39112 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003068774-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1437
ID   ABM34877 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003104538-A1.
PD   05-JUN-2003.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1438
ID   ABO51353 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003049781-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1439
ID   ABO04179 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003036158-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1440
ID   ABO10649 standard; protein; 178 AA.
DE   Human PRO polypeptide #271.
PN   US2003036151-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1441
ID   ABR77892 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003040067-A1.
PD   27-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1442
ID   ABR79102 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003054456-A1.
PD   20-MAR-2003.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
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  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1443
ID   ABO24196 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003054482-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1444
ID   ABR93960 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003054457-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1445
ID   ABM02003 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003059883-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1446
ID   ABM78426 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003049764-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1447
ID   ABR90215 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003073177-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1448
ID   ABM27741 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003064442-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1449
ID   ABM13342 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003064450-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1450
ID   ABO32045 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003068731-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1451
ID   ABM14257 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003068683-A1.
PD   10-APR-2003.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1452
ID   ABM08462 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003068754-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1453
ID   ABO40332 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003068681-A1.
PD   10-APR-2003.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1454
ID   ABM74767 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003096351-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1455
ID   ABM33962 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003096358-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1456
ID   ABM20421 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003104556-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1457
ID   ABO48913 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003049756-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1458
ID   ABR72978 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003036122-A1.
PD   20-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1459
ID   ABO15620 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003036121-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1460
ID   ABR85335 standard; protein; 178 AA.
DE   Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN   US2003040065-A1.
PD   27-FEB-2003.
  Query Match             20.4%;  Score 94;  DB 7;  Length 178;
  Best Local Similarity   43.9%;  Pred. No. 0.0033;
RESULT 1461
ID   ABO15315 standard; protein; 178 AA.
DE   Human secreted/transmembrane protein (PRO) #271.
PN   US2003044919-A1.
PD   06-MAR-2003.
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Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1462
ID ABO17450 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1463
ID ABM17739 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1464
ID ABR85640 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1465
ID ABM77206 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1466
ID ABO28385 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1467
ID ABM23166 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1468
ID ABM30486 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1469
ID ABM21946 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1470
ID ABM21641 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1471
ID ABM15172 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1472
ID ABO41247 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1473
ID ABO36977 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1474
ID ABO37587 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1475
ID ABM75377 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1476
ID ABM33657 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1477
ID ABO46412 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1478
ID ADA82977 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1479
ID ADB91706 standard; protein; 178 AA.
DE Human secreted protein #SEQ ID 652.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1480
ID ABM32011 standard; protein; 178 AA.

DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1481
ID ABM31401 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1482
ID ADB86285 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1483
ID ABM32316 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1484
ID ABM32621 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1485
ID ABM31706 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1486
ID ABM31096 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1487
ID ADD06015 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1488
ID ADG03010 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1489
ID ADG01717 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1490
ID ADF95892 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1491
ID ADF74108 standard; protein; 178 AA.
DE Human cell adhesion inhibitor protein disadherin.
PN JP2003174885-A.
PD 24-JUN-2003.
PA (KOKU-) KOKURITSU GAN CENT SOCHO.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1492
ID ADG12707 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1493
ID ADH09367 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1494
ID ADL33146 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1495
ID ADM30682 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1496
ID ADP65271 standard; protein; 178 AA.
DE Human FXYD domain-containing ion transport regulator 5, dysadherin.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1497
ID ADE74679 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 20.4%; Score 94; DB 8; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1498
ID ADE75291 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 20.4%; Score 94; DB 8; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1499
ID ADF96504 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 20.4%; Score 94; DB 8; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1500
ID ADG04775 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 8; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;

GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 12, 2006, 21:28:50 ; Search time 47 Seconds
(without alignments)
156.556 Million cell updates/sec

Title: US-10-063-557-50
Perfect score: 461
Sequence: 1 MERVTLALLLLAGLTALEAN.....HSPVPEKAIPLITPGSATTC 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	461	100.0	89	2	US-09-289-349-11	Sequence 11, Appl
2	461	100.0	89	2	US-09-991-181-262	Sequence 262, App
3	461	100.0	89	2	US-09-990-444-262	Sequence 262, App
4	461	100.0	89	2	US-09-997-333-262	Sequence 262, App
5	461	100.0	89	2	US-09-992-598-262	Sequence 262, App
6	276.5	60.0	88	2	US-09-724-864-58	Sequence 58, Appl
7	256.5	55.6	87	1	US-08-725-531-5	Sequence 5, Appli
8	256.5	55.6	87	1	US-08-738-127-5	Sequence 5, Appli
9	256.5	55.6	87	1	US-09-213-392-5	Sequence 5, Appli
10	256.5	55.6	87	1	US-09-083-661-5	Sequence 5, Appli
11	214.5	46.5	87	1	US-08-289-247B-4	Sequence 4, Appli
12	214.5	46.5	87	1	US-08-725-531-4	Sequence 4, Appli
13	214.5	46.5	87	1	US-08-738-127-4	Sequence 4, Appli
14	214.5	46.5	87	1	US-09-213-392-4	Sequence 4, Appli
15	214.5	46.5	87	1	US-09-083-661-4	Sequence 4, Appli
16	214.5	46.5	124	2	US-09-949-016-8238	Sequence 8238, Ap
17	214.5	46.5	124	2	US-09-949-016-8239	Sequence 8239, Ap
18	191.5	41.5	178	2	US-09-949-016-9028	Sequence 9028, Ap
19	191.5	41.5	178	2	US-09-949-016-9029	Sequence 9029, Ap
20	131	28.4	106	2	US-09-621-976-5338	Sequence 5338, Ap
21	131	28.4	107	2	US-09-621-976-5332	Sequence 5332, Ap
22	129	28.0	92	1	US-08-738-127-1	Sequence 1, Appli
23	129	28.0	92	2	US-09-247-155-120	Sequence 120, App
24	129	28.0	92	2	US-09-148-545-238	Sequence 238, App
25	129	28.0	92	2	US-09-621-011-238	Sequence 238, App
26	129	28.0	92	2	US-09-903-190-120	Sequence 120, App
27	129	28.0	93	2	US-09-148-545-183	Sequence 183, App
28	129	28.0	93	2	US-09-621-011-183	Sequence 183, App
29	126.5	27.4	92	1	US-08-725-531-3	Sequence 3, Appli
30	126.5	27.4	92	1	US-08-738-127-3	Sequence 3, Appli
31	126.5	27.4	92	1	US-09-213-392-3	Sequence 3, Appli
32	126.5	27.4	92	1	US-09-083-661-3	Sequence 3, Appli
33	121	26.2	70	2	US-09-148-545-269	Sequence 269, App
34	121	26.2	70	2	US-09-621-011-269	Sequence 269, App
35	112.5	24.4	95	1	US-08-725-531-1	Sequence 1, Appli
36	112.5	24.4	95	1	US-09-213-392-1	Sequence 1, Appli
37	112.5	24.4	95	1	US-09-083-661-1	Sequence 1, Appli
38	112.5	24.4	96	2	US-09-149-476-473	Sequence 473, App
39	112.5	24.4	120	2	US-09-991-181-199	Sequence 199, App
40	112.5	24.4	120	2	US-09-990-444-199	Sequence 199, App
41	112.5	24.4	120	2	US-09-997-333-199	Sequence 199, App
42	112.5	24.4	120	2	US-09-992-598-199	Sequence 199, App
43	106	23.0	69	2	US-09-149-476-606	Sequence 606, App
44	103.5	22.5	95	2	US-09-621-976-5250	Sequence 5250, Ap
45	99.5	21.6	72	2	US-08-905-223-405	Sequence 405, App
46	94	20.4	179	2	US-09-205-258-424	Sequence 424, App
47	94	20.4	179	2	US-10-004-860-424	Sequence 424, App
48	89	19.3	80	2	US-09-621-976-6085	Sequence 6085, Ap
49	83	18.0	86	2	US-09-949-016-8419	Sequence 8419, Ap
50	83	18.0	86	2	US-09-949-016-8420	Sequence 8420, Ap
51	73.5	15.9	58	1	US-08-725-531-6	Sequence 6, Appli
52	73.5	15.9	58	1	US-08-738-127-6	Sequence 6, Appli
53	73.5	15.9	58	1	US-09-213-392-6	Sequence 6, Appli
54	73.5	15.9	58	1	US-09-083-661-6	Sequence 6, Appli
55	67.5	14.6	664	2	US-09-268-140-2	Sequence 2, Appli
56	67.5	14.6	664	2	US-09-949-016-9005	Sequence 9005, Ap
57	66.5	14.4	376	2	US-09-198-452A-1112	Sequence 1112, Ap
58	66.5	14.4	388	2	US-09-438-185A-1038	Sequence 1038, Ap
59	66.5	14.4	523	2	US-09-949-016-6195	Sequence 6195, Ap
60	66.5	14.4	552	2	US-09-949-016-8164	Sequence 8164, Ap
61	64.5	14.0	729	2	US-09-248-796A-17121	Sequence 17121, A
62	63	13.7	627	2	US-10-222-100-3	Sequence 3, Appli
63	62.5	13.6	339	2	US-09-690-454-66	Sequence 66, Appl
64	62.5	13.6	340	2	US-09-690-454-174	Sequence 174, App
65	62.5	13.6	389	2	US-09-328-352-7324	Sequence 7324, Ap
66	62	13.4	78	2	US-09-749-637A-342	Sequence 342, App
67	62	13.4	360	2	US-09-489-039A-8000	Sequence 8000, Ap
68	62	13.4	601	2	US-09-336-643A-4	Sequence 4, Appli
69	61.5	13.3	103	2	US-09-107-532A-3725	Sequence 3725, Ap
70	61.5	13.3	433	2	US-09-198-452A-925	Sequence 925, App
71	61.5	13.3	453	2	US-09-438-185A-860	Sequence 860, App
72	61.5	13.3	549	2	US-09-120-365-3	Sequence 3, Appli
73	61.5	13.3	549	2	US-09-515-039-3	Sequence 3, Appli
74	61.5	13.3	606	2	US-09-270-767-41830	Sequence 41830, A
75	61.5	13.3	990	2	US-10-363-937-7	Sequence 7, Appli
76	61	13.2	457	2	US-09-489-039A-12762	Sequence 12762, A
77	60.5	13.1	106	2	US-09-149-476-341	Sequence 341, App
78	60.5	13.1	288	2	US-09-386-642-13	Sequence 13, Appl
79	60.5	13.1	998	2	US-09-252-991A-28424	Sequence 28424, A
80	60	13.0	234	2	US-09-248-796A-17625	Sequence 17625, A
81	60	13.0	337	2	US-08-930-830B-2	Sequence 2, Appli
82	60	13.0	342	2	US-08-930-830B-5	Sequence 5, Appli
83	60	13.0	404	2	US-09-949-016-7352	Sequence 7352, Ap
84	60	13.0	426	2	US-09-252-991A-27522	Sequence 27522, A
85	60	13.0	497	2	US-09-718-693A-1	Sequence 1, Appli
86	59	12.8	83	2	US-09-227-357-652	Sequence 652, App
87	59	12.8	83	2	US-09-973-278-370	Sequence 370, App
88	59	12.8	430	2	US-09-134-000C-4819	Sequence 4819, Ap
89	59	12.8	539	1	US-08-464-340A-13	Sequence 13, Appl
90	59	12.8	806	2	US-09-833-466-13	Sequence 13, Appl
91	59	12.8	854	2	US-09-833-466-12	Sequence 12, Appl
92	59	12.8	858	2	US-09-275-252A-6	Sequence 6, Appli
93	58.5	12.7	142	2	US-09-543-681A-5222	Sequence 5222, Ap
94	58.5	12.7	200	2	US-09-252-991A-27855	Sequence 27855, A
95	58.5	12.7	243	2	US-09-107-532A-4908	Sequence 4908, Ap
96	58.5	12.7	260	2	US-09-070-526-2	Sequence 2, Appli
97	58.5	12.7	260	2	US-09-618-259-7	Sequence 7, Appli
98	58.5	12.7	260	2	US-09-999-833A-395	Sequence 395, App
99	58.5	12.7	260	2	US-10-020-445A-395	Sequence 395, App
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103	58.5	12.7	383	2	US-08-530-862B-6	Sequence 6, Appli
104	58.5	12.7	383	2	US-08-597-313D-6	Sequence 6, Appli
105	58.5	12.7	383	2	US-09-059-769-9	Sequence 9, Appli
106	58.5	12.7	383	2	US-09-161-994A-14	Sequence 14, Appl
107	58.5	12.7	383	2	US-09-133-962A-2	Sequence 2, Appli
108	58.5	12.7	383	2	US-09-045-940-41	Sequence 41, Appl
109	58.5	12.7	383	2	US-09-763-331-4	Sequence 4, Appli
110	58.5	12.7	383	2	US-09-697-379-2	Sequence 2, Appli
111	58.5	12.7	383	2	US-10-116-212A-2	Sequence 2, Appli
112	58.5	12.7	383	2	US-09-885-189-6	Sequence 6, Appli
113	58.5	12.7	518	2	US-09-902-540-14949	Sequence 14949, A
114	58.5	12.7	1058	2	US-09-489-039A-11177	Sequence 11177, A
115	58	12.6	228	2	US-09-489-039A-10271	Sequence 10271, A
116	58	12.6	427	2	US-09-902-540-14326	Sequence 14326, A
117	58	12.6	681	2	US-10-104-047-3586	Sequence 3586, Ap
118	57.5	12.5	27	2	US-09-962-756-1644	Sequence 1644, Ap
119	57.5	12.5	352	2	US-09-252-991A-17455	Sequence 17455, A
120	57.5	12.5	471	2	US-09-252-991A-27897	Sequence 27897, A
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122	57.5	12.5	499	2	US-09-902-540-12205	Sequence 12205, A
123	57.5	12.5	528	1	US-08-527-152-2	Sequence 2, Appli
124	57.5	12.5	775	2	US-09-252-991A-28461	Sequence 28461, A
125	57.5	12.5	1107	2	US-09-489-039A-8890	Sequence 8890, Ap
126	57	12.4	185	2	US-10-018-924-6	Sequence 6, Appli
127	57	12.4	647	2	US-09-543-681A-5240	Sequence 5240, Ap
128	56.5	12.3	89	1	US-07-939-501A-2	Sequence 2, Appli
129	56.5	12.3	89	1	US-07-966-187-5	Sequence 5, Appli
130	56.5	12.3	89	1	US-08-371-121-4	Sequence 4, Appli
131	56.5	12.3	89	2	US-07-927-391-6	Sequence 6, Appli
132	56.5	12.3	89	2	US-08-115-753-15	Sequence 15, Appl
133	56.5	12.3	158	2	US-09-107-532A-6092	Sequence 6092, Ap
134	56.5	12.3	168	2	US-09-898-659-16	Sequence 16, Appl
135	56.5	12.3	205	2	US-08-818-112-80	Sequence 80, Appl
136	56.5	12.3	205	2	US-08-818-111-81	Sequence 81, Appl
137	56.5	12.3	205	2	US-09-056-556-80	Sequence 80, Appl
138	56.5	12.3	205	2	US-09-072-596-81	Sequence 81, Appl
139	56.5	12.3	205	2	US-09-072-967-80	Sequence 80, Appl
140	56.5	12.3	205	2	US-10-193-002-81	Sequence 81, Appl
141	56.5	12.3	205	2	US-10-084-843-80	Sequence 80, Appl
142	56.5	12.3	213	2	US-09-605-703B-2594	Sequence 2594, Ap
143	56.5	12.3	233	2	US-08-818-112-76	Sequence 76, Appl
144	56.5	12.3	233	2	US-08-818-111-77	Sequence 77, Appl
145	56.5	12.3	233	2	US-09-056-556-76	Sequence 76, Appl
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147	56.5	12.3	233	2	US-09-072-967-76	Sequence 76, Appl
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153	56.5	12.3	385	2	US-08-880-865-3	Sequence 3, Appli
154	56.5	12.3	419	2	US-08-115-753-2	Sequence 2, Appli
155	56.5	12.3	419	2	US-08-115-753-33	Sequence 33, Appl
156	56.5	12.3	601	2	US-09-949-016-9977	Sequence 9977, Ap
157	56.5	12.3	626	2	US-09-957-187-83	Sequence 83, Appl
158	56.5	12.3	630	2	US-09-520-781-30	Sequence 30, Appl
159	56.5	12.3	630	2	US-09-957-187-30	Sequence 30, Appl
160	56.5	12.3	630	2	US-09-991-053-30	Sequence 30, Appl
161	56.5	12.3	697	2	US-10-101-464A-940	Sequence 940, App
162	56.5	12.3	757	2	US-09-949-016-7121	Sequence 7121, Ap
163	56.5	12.3	852	1	US-08-190-802A-59	Sequence 59, Appl
164	56.5	12.3	852	1	US-08-190-802A-67	Sequence 67, Appl
165	56.5	12.3	852	2	US-08-477-346-59	Sequence 59, Appl
166	56.5	12.3	852	2	US-08-477-346-67	Sequence 67, Appl
167	56.5	12.3	852	2	US-08-473-089-59	Sequence 59, Appl
168	56.5	12.3	852	2	US-08-473-089-67	Sequence 67, Appl
169	56.5	12.3	852	2	US-08-487-072A-59	Sequence 59, Appl
170	56.5	12.3	852	2	US-08-487-072A-67	Sequence 67, Appl
171	56.5	12.3	884	2	US-09-520-781-6	Sequence 6, Appli
172	56.5	12.3	884	2	US-09-957-187-6	Sequence 6, Appli
173	56.5	12.3	884	2	US-09-991-053-6	Sequence 6, Appli
174	56.5	12.3	939	2	US-09-520-781-4	Sequence 4, Appli
175	56.5	12.3	939	2	US-09-957-187-4	Sequence 4, Appli
176	56.5	12.3	939	2	US-09-991-053-4	Sequence 4, Appli
177	56.5	12.3	1030	2	US-09-856-681A-2	Sequence 2, Appli
178	56.5	12.3	1030	2	US-09-856-681A-7	Sequence 7, Appli
179	56.5	12.3	1047	2	US-09-957-187-85	Sequence 85, Appl
180	56	12.1	199	2	US-09-543-681A-5720	Sequence 5720, Ap
181	56	12.1	202	2	US-09-489-039A-8619	Sequence 8619, Ap
182	56	12.1	316	2	US-09-540-236-3467	Sequence 3467, Ap
183	56	12.1	579	2	US-09-540-236-2071	Sequence 2071, Ap
184	56	12.1	593	2	US-09-949-016-10355	Sequence 10355, A
185	56	12.1	605	2	US-09-252-991A-24349	Sequence 24349, A
186	56	12.1	1058	2	US-09-949-016-11457	Sequence 11457, A
187	56	12.1	1384	2	US-08-826-134-2	Sequence 2, Appli
188	56	12.1	1384	2	US-09-949-016-6395	Sequence 6395, Ap
189	56	12.1	1633	2	US-09-902-540-12892	Sequence 12892, A
190	56	12.1	1805	2	US-09-949-016-8246	Sequence 8246, Ap
191	55.5	12.0	175	2	US-09-252-991A-32945	Sequence 32945, A
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193	55.5	12.0	248	1	US-08-303-651-2	Sequence 2, Appli
194	55.5	12.0	248	2	US-08-767-993-3	Sequence 3, Appli
195	55.5	12.0	262	1	US-08-313-553-2	Sequence 2, Appli
196	55.5	12.0	262	2	US-08-767-993-2	Sequence 2, Appli
197	55.5	12.0	292	1	US-08-555-568B-19	Sequence 19, Appl
198	55.5	12.0	292	2	US-09-519-223-19	Sequence 19, Appl
199	55.5	12.0	292	2	US-09-927-180-19	Sequence 19, Appl
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201	55.5	12.0	384	1	US-08-675-650B-2	Sequence 2, Appli
202	55.5	12.0	384	2	US-09-354-231B-14	Sequence 14, Appl
203	55.5	12.0	384	2	US-09-354-231B-16	Sequence 16, Appl
204	55.5	12.0	384	2	US-09-354-231B-18	Sequence 18, Appl
205	55.5	12.0	384	2	US-09-128-602B-14	Sequence 14, Appl
206	55.5	12.0	384	2	US-09-128-602B-16	Sequence 16, Appl
207	55.5	12.0	384	2	US-09-128-602B-18	Sequence 18, Appl
208	55.5	12.0	384	2	US-09-995-297-14	Sequence 14, Appl
209	55.5	12.0	384	2	US-09-995-297-16	Sequence 16, Appl
210	55.5	12.0	384	2	US-09-995-297-18	Sequence 18, Appl
211	55.5	12.0	391	2	US-09-489-039A-9791	Sequence 9791, Ap
212	55.5	12.0	445	4	PCT-US94-05387-7	Sequence 7, Appli
213	55.5	12.0	559	1	US-08-313-553-15	Sequence 15, Appl
214	55.5	12.0	559	2	US-08-767-993-15	Sequence 15, Appl
215	55.5	12.0	687	1	US-08-555-568B-21	Sequence 21, Appl
216	55.5	12.0	687	2	US-09-519-223-21	Sequence 21, Appl
217	55.5	12.0	687	2	US-09-927-180-21	Sequence 21, Appl
218	55.5	12.0	688	1	US-08-555-568B-23	Sequence 23, Appl
219	55.5	12.0	688	2	US-09-519-223-23	Sequence 23, Appl
220	55.5	12.0	688	2	US-09-927-180-23	Sequence 23, Appl
221	55.5	12.0	819	2	US-09-949-016-10948	Sequence 10948, A
222	55.5	12.0	887	2	US-09-077-940A-2	Sequence 2, Appli
223	55.5	12.0	888	2	US-09-077-940A-4	Sequence 4, Appli
224	55.5	12.0	968	2	US-09-228-986-76	Sequence 76, Appl
225	55.5	12.0	968	2	US-10-101-464A-76	Sequence 76, Appl
226	55	11.9	124	2	US-09-270-767-33906	Sequence 33906, A
227	55	11.9	124	2	US-09-270-767-49123	Sequence 49123, A
228	55	11.9	205	2	US-09-248-796A-15224	Sequence 15224, A
229	55	11.9	232	1	US-08-456-670B-39	Sequence 39, Appl
230	55	11.9	232	2	US-09-372-036-39	Sequence 39, Appl
231	55	11.9	359	2	US-09-248-796A-18202	Sequence 18202, A
232	55	11.9	376	2	US-09-103-331-42	Sequence 42, Appl
233	55	11.9	376	2	US-09-631-594-51	Sequence 51, Appl
234	55	11.9	381	2	US-09-248-796A-19630	Sequence 19630, A
235	55	11.9	404	2	US-09-538-092-50	Sequence 50, Appl
236	55	11.9	406	2	US-09-252-991A-20630	Sequence 20630, A
237	55	11.9	459	2	US-08-311-731A-47	Sequence 47, Appl
238	55	11.9	478	1	US-08-456-670B-40	Sequence 40, Appl
239	55	11.9	478	2	US-09-372-036-40	Sequence 40, Appl
240	55	11.9	484	1	US-08-127-499A-26	Sequence 26, Appl
241	55	11.9	484	1	US-08-482-847-26	Sequence 26, Appl
242	55	11.9	512	1	US-08-173-508-4	Sequence 4, Appli
243	55	11.9	512	1	US-08-265-310-4	Sequence 4, Appli
244	55	11.9	512	2	US-08-951-742-4	Sequence 4, Appli
245	55	11.9	533	2	US-09-549-519-32	Sequence 32, Appl
246	55	11.9	598	2	US-09-252-991A-25875	Sequence 25875, A

247	55	11.9	666	1	US-08-083-590A-17	Sequence 17, Appl
248	55	11.9	666	1	US-08-346-128-36	Sequence 36, Appl
249	55	11.9	666	2	US-08-532-384-17	Sequence 17, Appl
250	55	11.9	1481	1	US-08-616-844-40	Sequence 40, Appl
251	55	11.9	1481	1	US-08-599-654-40	Sequence 40, Appl
252	55	11.9	1481	2	US-08-944-868A-40	Sequence 40, Appl
253	55	11.9	1481	2	US-08-944-423A-40	Sequence 40, Appl
254	55	11.9	1481	2	US-08-944-496-40	Sequence 40, Appl
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258	54.5	11.8	221	2	US-09-270-767-31937	Sequence 31937, A
259	54.5	11.8	221	2	US-09-270-767-47154	Sequence 47154, A
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271	54.5	11.8	384	2	US-09-128-602B-4	Sequence 4, Appli
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273	54.5	11.8	384	2	US-09-482-287-4	Sequence 4, Appli
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277	54.5	11.8	384	2	US-09-995-297-4	Sequence 4, Appli
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287	54.5	11.8	752	1	US-08-555-568B-2	Sequence 2, Appli
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289	54.5	11.8	752	2	US-09-927-180-2	Sequence 2, Appli
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291	54.5	11.8	765	2	US-09-949-016-7844	Sequence 7844, Ap
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294	54.5	11.8	895	1	US-08-123-161A-8	Sequence 8, Appli
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296	54.5	11.8	895	2	US-09-949-016-6490	Sequence 6490, Ap
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300	54	11.7	135	4	PCT-US95-01087-6	Sequence 6, Appli
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311	54	11.7	346	2	US-09-736-457-329	Sequence 329, App
312	54	11.7	346	2	US-09-614-124B-329	Sequence 329, App
313	54	11.7	346	2	US-09-671-325-329	Sequence 329, App
314	54	11.7	346	2	US-09-589-184-329	Sequence 329, App
315	54	11.7	346	2	US-09-658-824-329	Sequence 329, App
316	54	11.7	346	2	US-10-017-754-329	Sequence 329, App
317	54	11.7	346	2	US-09-651-563-329	Sequence 329, App
318	54	11.7	346	2	US-09-519-642-329	Sequence 329, App
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324	54	11.7	397	4	PCT-US94-07280-11	Sequence 11, Appl
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327	54	11.7	410	4	PCT-US94-07280-18	Sequence 18, Appl
328	54	11.7	410	4	PCT-US95-01087-18	Sequence 18, Appl
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332	54	11.7	417	4	PCT-US95-01087-19	Sequence 19, Appl
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340	54	11.7	443	2	US-10-012-542-147	Sequence 147, App
341	54	11.7	443	2	US-10-115-123-147	Sequence 147, App
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344	54	11.7	447	4	PCT-US95-01087-20	Sequence 20, Appl
345	54	11.7	453	1	US-08-188-281B-16	Sequence 16, Appl
346	54	11.7	453	4	PCT-US94-07280-16	Sequence 16, Appl
347	54	11.7	453	4	PCT-US95-01087-16	Sequence 16, Appl
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349	54	11.7	490	1	US-08-188-281B-15	Sequence 15, Appl
350	54	11.7	490	4	PCT-US94-07280-15	Sequence 15, Appl
351	54	11.7	490	4	PCT-US95-01087-15	Sequence 15, Appl
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353	54	11.7	518	2	US-09-540-236-3648	Sequence 3648, Ap
354	54	11.7	880	2	US-09-538-092-601	Sequence 601, App
355	54	11.7	891	2	US-09-252-991A-28689	Sequence 28689, A
356	54	11.7	1036	2	US-09-902-540-14218	Sequence 14218, A
357	54	11.7	3623	2	US-09-341-461-2	Sequence 2, Appli
358	53.5	11.6	72	2	US-09-188-930-182	Sequence 182, App
359	53.5	11.6	221	2	US-09-464-535-22	Sequence 22, Appl
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361	53.5	11.6	244	2	US-09-618-259-11	Sequence 11, Appl
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363	53.5	11.6	284	2	US-09-902-540-16417	Sequence 16417, A
364	53.5	11.6	302	2	US-09-252-991A-21655	Sequence 21655, A
365	53.5	11.6	308	2	US-09-489-039A-14278	Sequence 14278, A
366	53.5	11.6	310	2	US-09-107-433-4601	Sequence 4601, Ap
367	53.5	11.6	325	2	US-09-949-016-7713	Sequence 7713, Ap
368	53.5	11.6	359	2	US-08-637-670-37	Sequence 37, Appl
369	53.5	11.6	382	2	US-09-489-039A-13696	Sequence 13696, A
370	53.5	11.6	407	2	US-09-710-279-1578	Sequence 1578, Ap
371	53.5	11.6	410	1	US-08-723-415B-10	Sequence 10, Appl
372	53.5	11.6	410	2	US-09-189-627A-10	Sequence 10, Appl
373	53.5	11.6	410	2	US-09-710-861-10	Sequence 10, Appl
374	53.5	11.6	415	2	US-09-949-016-8808	Sequence 8808, Ap
375	53.5	11.6	437	2	US-09-350-841A-1591	Sequence 1591, Ap
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377	53.5	11.6	438	2	US-08-360-107A-115	Sequence 115, App
378	53.5	11.6	438	2	US-08-484-223B-105	Sequence 105, App
379	53.5	11.6	438	2	US-08-919-597-105	Sequence 105, App
380	53.5	11.6	438	2	US-08-475-668A-105	Sequence 105, App
381	53.5	11.6	438	2	US-08-485-551A-105	Sequence 105, App
382	53.5	11.6	438	2	US-08-471-913A-105	Sequence 105, App
383	53.5	11.6	438	2	US-08-485-264A-105	Sequence 105, App
384	53.5	11.6	438	2	US-08-474-349A-105	Sequence 105, App
385	53.5	11.6	438	2	US-08-470-896-105	Sequence 105, App
386	53.5	11.6	438	2	US-08-485-546A-105	Sequence 105, App
387	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, App
388	53.5	11.6	438	2	US-08-484-741-105	Sequence 105, App
389	53.5	11.6	440	2	US-09-134-001C-3286	Sequence 3286, Ap
390	53.5	11.6	495	2	US-09-275-252A-5	Sequence 5, Appli
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392	53.5	11.6	550	2	US-09-230-944-18	Sequence 18, Appl

393	53.5	11.6	550	2	US-09-230-944-20	Sequence 20, Appl
394	53.5	11.6	550	2	US-09-873-233A-18	Sequence 18, Appl
395	53.5	11.6	550	2	US-09-873-233A-20	Sequence 20, Appl
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399	53	11.5	78	2	US-09-749-637A-228	Sequence 228, App
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401	53	11.5	223	2	US-09-605-703B-2326	Sequence 2326, Ap
402	53	11.5	225	2	US-09-543-681A-4579	Sequence 4579, Ap
403	53	11.5	239	2	US-08-913-014A-2	Sequence 2, Appli
404	53	11.5	239	2	US-09-653-285-2	Sequence 2, Appli
405	53	11.5	299	2	US-09-252-991A-24215	Sequence 24215, A
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417	53	11.5	474	2	US-09-489-039A-10791	Sequence 10791, A
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422	53	11.5	563	2	US-09-949-016-8277	Sequence 8277, Ap
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424	53	11.5	580	2	US-09-489-039A-8096	Sequence 8096, Ap
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431	53	11.5	896	2	US-10-270-878-17	Sequence 17, Appl
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435	53	11.5	1238	2	US-09-904-065-2	Sequence 2, Appli
436	53	11.5	1238	2	US-09-904-065-14	Sequence 14, Appl
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439	53	11.5	1240	2	US-09-904-065-15	Sequence 15, Appl
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442	53	11.5	1478	2	US-09-949-016-8315	Sequence 8315, Ap
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445	52.5	11.4	71	2	US-10-062-548-79	Sequence 79, Appl
446	52.5	11.4	123	2	US-09-107-532A-4652	Sequence 4652, Ap
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448	52.5	11.4	126	2	US-09-494-151-9	Sequence 9, Appli
449	52.5	11.4	126	2	US-09-972-484-9	Sequence 9, Appli
450	52.5	11.4	158	2	US-09-464-535-8	Sequence 8, Appli
451	52.5	11.4	167	2	US-09-438-185A-132	Sequence 132, App
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455	52.5	11.4	251	2	US-09-494-151-59	Sequence 59, Appl
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459	52.5	11.4	384	2	US-09-354-231B-8	Sequence 8, Appli
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468	52.5	11.4	384	2	US-09-966-888-6	Sequence 6, Appli
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478	52.5	11.4	410	1	US-08-602-846-2	Sequence 2, Appli
479	52.5	11.4	410	2	US-09-078-596-2	Sequence 2, Appli
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487	52.5	11.4	525	2	US-08-888-949-16	Sequence 16, Appl
488	52.5	11.4	525	2	US-08-888-950-16	Sequence 16, Appl
489	52.5	11.4	525	2	US-09-262-758-16	Sequence 16, Appl
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494	52.5	11.4	550	2	US-09-515-039-1	Sequence 1, Appli
495	52.5	11.4	609	2	US-09-107-532A-5110	Sequence 5110, Ap
496	52.5	11.4	693	2	US-09-949-016-9666	Sequence 9666, Ap
497	52.5	11.4	706	2	US-09-252-991A-25730	Sequence 25730, A
498	52.5	11.4	763	2	US-10-104-047-2766	Sequence 2766, Ap
499	52.5	11.4	800	2	US-09-489-039A-10358	Sequence 10358, A
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501	52.5	11.4	969	2	US-09-321-987B-5	Sequence 5, Appli
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503	52.5	11.4	1000	2	US-09-352-168-25	Sequence 25, Appl
504	52.5	11.4	1000	2	US-09-771-045B-25	Sequence 25, Appl
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506	52.5	11.4	1000	2	US-09-658-835C-25	Sequence 25, Appl
507	52.5	11.4	1101	2	US-08-331-625A-52	Sequence 52, Appl
508	52.5	11.4	1101	2	US-08-331-625A-54	Sequence 54, Appl
509	52.5	11.4	1101	2	US-09-494-151-52	Sequence 52, Appl
510	52.5	11.4	1101	2	US-09-494-151-54	Sequence 54, Appl
511	52.5	11.4	1101	2	US-09-972-484-52	Sequence 52, Appl
512	52.5	11.4	1101	2	US-09-972-484-54	Sequence 54, Appl
513	52.5	11.4	1205	2	US-09-491-522-11	Sequence 11, Appl
514	52.5	11.4	1279	2	US-09-489-039A-13602	Sequence 13602, A
515	52.5	11.4	1452	2	US-08-331-625A-2	Sequence 2, Appli
516	52.5	11.4	1452	2	US-09-494-151-2	Sequence 2, Appli
517	52.5	11.4	1452	2	US-09-972-484-2	Sequence 2, Appli
518	52.5	11.4	1452	4	PCT-US93-04384-18	Sequence 18, Appl
519	52.5	11.4	1452	4	PCT-US93-04692-2	Sequence 2, Appli
520	52.5	11.4	1453	1	US-08-308-872B-6	Sequence 6, Appli
521	52.5	11.4	2037	2	US-09-306-998-3	Sequence 3, Appli
522	52.5	11.4	2046	2	US-09-949-016-9365	Sequence 9365, Ap
523	52	11.3	87	2	US-09-252-991A-17552	Sequence 17552, A
524	52	11.3	105	2	US-09-288-143-209	Sequence 209, App
525	52	11.3	127	2	US-09-328-352-4209	Sequence 4209, Ap
526	52	11.3	132	2	US-09-454-279-6	Sequence 6, Appli
527	52	11.3	136	2	US-09-270-767-39814	Sequence 39814, A
528	52	11.3	136	2	US-09-270-767-55031	Sequence 55031, A
529	52	11.3	160	2	US-09-583-110-5206	Sequence 5206, Ap
530	52	11.3	161	2	US-09-107-433-3565	Sequence 3565, Ap
531	52	11.3	175	2	US-09-270-767-46710	Sequence 46710, A
532	52	11.3	216	2	US-09-107-532A-3711	Sequence 3711, Ap
533	52	11.3	231	2	US-09-303-518D-432	Sequence 432, App
534	52	11.3	260	2	US-09-025-059-3	Sequence 3, Appli
535	52	11.3	260	2	US-08-888-429A-26	Sequence 26, Appl
536	52	11.3	260	2	US-09-593-653-26	Sequence 26, Appl
537	52	11.3	260	2	US-09-618-259-8	Sequence 8, Appli
538	52	11.3	261	2	US-09-454-279-16	Sequence 16, Appl

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540	52	11.3	267	2	US-09-248-796A-17580	Sequence 17580, A
541	52	11.3	304	2	US-09-543-681A-7290	Sequence 7290, Ap
542	52	11.3	312	2	US-09-543-681A-6689	Sequence 6689, Ap
543	52	11.3	336	2	US-09-902-540-10582	Sequence 10582, A
544	52	11.3	350	2	US-09-543-681A-4618	Sequence 4618, Ap
545	52	11.3	371	2	US-09-949-016-8635	Sequence 8635, Ap
546	52	11.3	380	2	US-08-888-429A-30	Sequence 30, Appl
547	52	11.3	380	2	US-09-593-653-30	Sequence 30, Appl
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549	52	11.3	389	2	US-08-888-429A-20	Sequence 20, Appl
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555	52	11.3	419	2	US-09-206-166-5	Sequence 5, Appli
556	52	11.3	419	2	US-09-593-653-28	Sequence 28, Appl
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558	52	11.3	433	2	US-09-949-016-7636	Sequence 7636, Ap
559	52	11.3	435	2	US-09-446-754-2	Sequence 2, Appli
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563	52	11.3	468	2	US-09-446-754-10	Sequence 10, Appl
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567	52	11.3	596	2	US-09-134-001C-3363	Sequence 3363, Ap
568	52	11.3	628	2	US-09-602-787A-550	Sequence 550, App
569	52	11.3	628	2	US-09-602-787A-666	Sequence 666, App
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572	52	11.3	1195	2	US-09-949-016-6535	Sequence 6535, Ap
573	52	11.3	1666	2	US-09-949-016-8322	Sequence 8322, Ap
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575	52	11.3	1956	2	US-09-527-013-2	Sequence 2, Appli
576	52	11.3	1957	2	US-08-669-656A-2	Sequence 2, Appli
577	52	11.3	1957	2	US-08-669-656A-8	Sequence 8, Appli
578	52	11.3	2057	2	US-09-499-203-2	Sequence 2, Appli
579	52	11.3	2132	2	US-08-669-656A-6	Sequence 6, Appli
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583	51.5	11.2	123	2	US-08-485-388-19	Sequence 19, Appl
584	51.5	11.2	123	2	US-08-474-853-19	Sequence 19, Appl
585	51.5	11.2	123	2	US-09-166-205B-19	Sequence 19, Appl
586	51.5	11.2	123	2	US-10-104-047-2234	Sequence 2234, Ap
587	51.5	11.2	123	4	PCT-US94-02629-19	Sequence 19, Appl
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592	51.5	11.2	211	2	US-09-603-552-12	Sequence 12, Appl
593	51.5	11.2	211	2	US-09-886-683A-4	Sequence 4, Appli
594	51.5	11.2	211	2	US-09-949-016-6992	Sequence 6992, Ap
595	51.5	11.2	211	2	US-09-999-833A-270	Sequence 270, App
596	51.5	11.2	211	2	US-10-020-445A-270	Sequence 270, App
597	51.5	11.2	212	1	US-08-461-859-35	Sequence 35, Appl
598	51.5	11.2	212	2	US-09-917-254-62	Sequence 62, Appl
599	51.5	11.2	224	2	US-08-871-572B-13	Sequence 13, Appl
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604	51.5	11.2	268	2	US-09-818-780-17	Sequence 17, Appl
605	51.5	11.2	268	2	US-09-818-780-94	Sequence 94, Appl
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607	51.5	11.2	292	2	US-10-004-860-1116	Sequence 1116, Ap
608	51.5	11.2	307	2	US-09-107-433-4181	Sequence 4181, Ap
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610	51.5	11.2	307	2	US-10-015-389A-95	Sequence 95, Appl
611	51.5	11.2	307	2	US-10-006-768A-95	Sequence 95, Appl
612	51.5	11.2	307	2	US-10-015-671A-95	Sequence 95, Appl
613	51.5	11.2	307	2	US-10-015-393A-95	Sequence 95, Appl
614	51.5	11.2	307	2	US-10-011-833A-95	Sequence 95, Appl
615	51.5	11.2	307	2	US-10-006-041A-95	Sequence 95, Appl
616	51.5	11.2	307	2	US-10-012-064A-95	Sequence 95, Appl
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619	51.5	11.2	334	4	PCT-US93-08528-73	Sequence 73, Appl
620	51.5	11.2	369	1	US-08-416-756A-2	Sequence 2, Appli
621	51.5	11.2	369	2	US-08-880-865-2	Sequence 2, Appli
622	51.5	11.2	371	2	US-09-949-016-9073	Sequence 9073, Ap
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624	51.5	11.2	381	1	US-08-467-948A-28	Sequence 28, Appl
625	51.5	11.2	381	2	US-08-852-824-18	Sequence 18, Appl
626	51.5	11.2	381	2	US-08-467-947A-28	Sequence 28, Appl
627	51.5	11.2	381	2	US-09-731-030A-17	Sequence 17, Appl
628	51.5	11.2	381	2	US-09-518-383-18	Sequence 18, Appl
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630	51.5	11.2	382	2	US-09-542-733-2	Sequence 2, Appli
631	51.5	11.2	382	2	US-09-262-477-2	Sequence 2, Appli
632	51.5	11.2	382	2	US-09-169-205D-21	Sequence 21, Appl
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634	51.5	11.2	383	1	US-08-760-936-4	Sequence 4, Appli
635	51.5	11.2	383	2	US-09-225-024-4	Sequence 4, Appli
636	51.5	11.2	384	2	US-08-530-862B-4	Sequence 4, Appli
637	51.5	11.2	384	2	US-08-597-313D-4	Sequence 4, Appli
638	51.5	11.2	384	2	US-09-885-189-4	Sequence 4, Appli
639	51.5	11.2	390	1	US-08-416-756A-5	Sequence 5, Appli
640	51.5	11.2	390	2	US-08-880-865-5	Sequence 5, Appli
641	51.5	11.2	407	2	US-08-753-007A-6	Sequence 6, Appli
642	51.5	11.2	407	2	US-09-398-496-6	Sequence 6, Appli
643	51.5	11.2	429	2	US-08-311-731A-287	Sequence 287, App
644	51.5	11.2	453	2	US-09-540-236-3464	Sequence 3464, Ap
645	51.5	11.2	495	2	US-09-270-767-44726	Sequence 44726, A
646	51.5	11.2	509	2	US-08-845-546-2	Sequence 2, Appli
647	51.5	11.2	511	2	US-09-252-991A-27306	Sequence 27306, A
648	51.5	11.2	522	2	US-09-549-519-40	Sequence 40, Appl
649	51.5	11.2	549	2	US-09-345-473E-32	Sequence 32, Appl
650	51.5	11.2	549	2	US-09-862-027-32	Sequence 32, Appl
651	51.5	11.2	550	1	US-08-348-891A-5	Sequence 5, Appli
652	51.5	11.2	550	1	US-08-905-817-5	Sequence 5, Appli
653	51.5	11.2	550	2	US-10-149-634-4	Sequence 4, Appli
654	51.5	11.2	563	2	US-10-046-232-24	Sequence 24, Appl
655	51.5	11.2	567	2	US-09-252-991A-28481	Sequence 28481, A
656	51.5	11.2	586	2	US-09-489-039A-10912	Sequence 10912, A
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659	51.5	11.2	707	2	US-10-101-464A-80	Sequence 80, Appl
660	51.5	11.2	760	2	US-09-589-892B-11	Sequence 11, Appl
661	51.5	11.2	808	2	US-10-104-047-2654	Sequence 2654, Ap
662	51.5	11.2	848	2	US-08-976-255-10	Sequence 10, Appl
663	51.5	11.2	869	1	US-08-483-101-15	Sequence 15, Appl
664	51.5	11.2	1451	1	US-08-308-872B-4	Sequence 4, Appli
665	51.5	11.2	1454	2	US-08-392-459-32	Sequence 32, Appl
666	51.5	11.2	1454	2	US-09-854-799-32	Sequence 32, Appl
667	51.5	11.2	1454	4	PCT-US91-08525-32	Sequence 32, Appl
668	51.5	11.2	1454	4	PCT-US93-04384-12	Sequence 12, Appl
669	51.5	11.2	1454	4	PCT-US93-04384-44	Sequence 44, Appl
670	51.5	11.2	1454	4	PCT-US93-04384-46	Sequence 46, Appl
671	51.5	11.2	1454	4	PCT-US93-04384-47	Sequence 47, Appl
672	51.5	11.2	2539	2	US-09-413-814-42	Sequence 42, Appl
673	51	11.1	86	2	US-08-654-737B-2	Sequence 2, Appli
674	51	11.1	109	2	US-09-198-452A-11	Sequence 11, Appl
675	51	11.1	109	2	US-09-438-185A-2	Sequence 2, Appli
676	51	11.1	119	2	US-09-270-767-32131	Sequence 32131, A
677	51	11.1	141	2	US-09-543-681A-6396	Sequence 6396, Ap
678	51	11.1	205	2	US-09-605-703B-1998	Sequence 1998, Ap
679	51	11.1	211	2	US-09-248-796A-20685	Sequence 20685, A
680	51	11.1	214	1	US-08-277-231A-14	Sequence 14, Appl
681	51	11.1	214	1	US-08-473-750-3	Sequence 3, Appli
682	51	11.1	214	1	US-08-477-326-3	Sequence 3, Appli
683	51	11.1	217	1	US-08-277-231A-2	Sequence 2, Appli
684	51	11.1	217	1	US-08-277-231A-12	Sequence 12, Appl

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687	51	11.1	217	1	US-08-477-326-1	Sequence 1, Appli
688	51	11.1	217	1	US-08-477-326-5	Sequence 5, Appli
689	51	11.1	222	2	US-09-252-991A-29014	Sequence 29014, A
690	51	11.1	230	2	US-09-328-352-7370	Sequence 7370, Ap
691	51	11.1	294	2	US-09-252-991A-27242	Sequence 27242, A
692	51	11.1	301	2	US-09-489-039A-12748	Sequence 12748, A
693	51	11.1	320	2	US-09-902-540-12563	Sequence 12563, A
694	51	11.1	321	2	US-09-290-586A-22	Sequence 22, Appl
695	51	11.1	326	2	US-09-489-039A-11901	Sequence 11901, A
696	51	11.1	328	2	US-09-489-039A-10986	Sequence 10986, A
697	51	11.1	330	2	US-09-134-001C-3815	Sequence 3815, Ap
698	51	11.1	338	2	US-09-949-016-8751	Sequence 8751, Ap
699	51	11.1	346	2	US-08-888-429A-18	Sequence 18, Appl
700	51	11.1	346	2	US-09-198-452A-60	Sequence 60, Appl
701	51	11.1	346	2	US-09-593-653-18	Sequence 18, Appl
702	51	11.1	354	2	US-09-902-540-15411	Sequence 15411, A
703	51	11.1	361	1	US-08-390-162-4	Sequence 4, Appli
704	51	11.1	361	1	US-08-685-945B-4	Sequence 4, Appli
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706	51	11.1	365	1	US-08-685-945B-2	Sequence 2, Appli
707	51	11.1	365	2	US-09-949-016-9075	Sequence 9075, Ap
708	51	11.1	370	2	US-09-489-039A-11515	Sequence 11515, A
709	51	11.1	380	2	US-09-902-540-15775	Sequence 15775, A
710	51	11.1	383	2	US-08-530-862B-7	Sequence 7, Appli
711	51	11.1	384	2	US-08-597-313D-7	Sequence 7, Appli
712	51	11.1	384	2	US-09-885-189-7	Sequence 7, Appli
713	51	11.1	430	2	US-09-902-540-12684	Sequence 12684, A
714	51	11.1	438	2	US-09-107-532A-5677	Sequence 5677, Ap
715	51	11.1	451	2	US-09-489-039A-8949	Sequence 8949, Ap
716	51	11.1	475	2	US-09-489-039A-8862	Sequence 8862, Ap
717	51	11.1	485	2	US-10-140-372-12	Sequence 12, Appl
718	51	11.1	485	2	US-09-438-185A-43	Sequence 43, Appl
719	51	11.1	490	2	US-09-438-185A-1032	Sequence 1032, Ap
720	51	11.1	534	2	US-09-605-703B-1142	Sequence 1142, Ap
721	51	11.1	584	2	US-09-107-532A-4564	Sequence 4564, Ap
722	51	11.1	590	2	US-09-248-796A-26874	Sequence 26874, A
723	51	11.1	598	2	US-09-248-796A-19190	Sequence 19190, A
724	51	11.1	677	2	US-09-252-991A-20406	Sequence 20406, A
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726	51	11.1	749	2	US-09-250-083C-2	Sequence 2, Appli
727	51	11.1	822	2	US-09-248-796A-19917	Sequence 19917, A
728	51	11.1	866	1	US-08-386-727-8	Sequence 8, Appli
729	51	11.1	866	1	US-08-600-452A-8	Sequence 8, Appli
730	51	11.1	954	2	US-09-854-845-14	Sequence 14, Appl
731	51	11.1	967	2	US-09-139-802-201	Sequence 201, App
732	51	11.1	967	2	US-09-659-786-201	Sequence 201, App
733	51	11.1	1049	2	US-09-854-845-2	Sequence 2, Appli
734	51	11.1	1093	2	US-09-854-845-4	Sequence 4, Appli
735	51	11.1	1151	2	US-09-854-845-10	Sequence 10, Appl
736	51	11.1	1479	2	US-08-840-062-4	Sequence 4, Appli
737	51	11.1	1956	2	US-08-843-417-10	Sequence 10, Appl
738	51	11.1	1956	2	US-09-527-013-10	Sequence 10, Appl
739	50.5	11.0	26	2	US-09-962-756-1658	Sequence 1658, Ap
740	50.5	11.0	87	2	US-09-605-703B-960	Sequence 960, App
741	50.5	11.0	87	2	US-09-605-703B-962	Sequence 962, App
742	50.5	11.0	142	2	US-10-104-047-2706	Sequence 2706, Ap
743	50.5	11.0	147	2	US-09-543-681A-4506	Sequence 4506, Ap
744	50.5	11.0	188	1	US-08-160-524A-5	Sequence 5, Appli
745	50.5	11.0	207	1	US-08-609-443B-15	Sequence 15, Appl
746	50.5	11.0	207	1	US-08-569-063C-15	Sequence 15, Appl
747	50.5	11.0	207	2	US-08-851-896-15	Sequence 15, Appl
748	50.5	11.0	249	2	US-09-583-110-4357	Sequence 4357, Ap
749	50.5	11.0	249	2	US-09-602-777A-344	Sequence 344, App
750	50.5	11.0	254	2	US-09-107-433-4333	Sequence 4333, Ap
751	50.5	11.0	255	2	US-09-605-703B-244	Sequence 244, App
752	50.5	11.0	263	2	US-09-605-703B-242	Sequence 242, App
753	50.5	11.0	264	1	US-08-463-115-93	Sequence 93, Appl
754	50.5	11.0	264	1	US-08-465-388-93	Sequence 93, Appl
755	50.5	11.0	271	2	US-09-252-991A-18965	Sequence 18965, A
756	50.5	11.0	304	2	US-09-902-540-13353	Sequence 13353, A
757	50.5	11.0	306	2	US-09-252-991A-22181	Sequence 22181, A
758	50.5	11.0	326	2	US-09-328-352-5506	Sequence 5506, Ap
759	50.5	11.0	349	2	US-09-949-016-9786	Sequence 9786, Ap
760	50.5	11.0	355	2	US-08-984-618-14	Sequence 14, Appl
761	50.5	11.0	364	2	US-09-829-275-1	Sequence 1, Appli
762	50.5	11.0	377	1	US-08-188-277B-2	Sequence 2, Appli
763	50.5	11.0	377	1	US-08-429-964-80	Sequence 80, Appl
764	50.5	11.0	385	2	US-09-107-532A-5871	Sequence 5871, Ap
765	50.5	11.0	411	2	US-09-107-532A-6966	Sequence 6966, Ap
766	50.5	11.0	424	2	US-09-902-540-10575	Sequence 10575, A
767	50.5	11.0	426	2	US-09-902-540-14942	Sequence 14942, A
768	50.5	11.0	433	2	US-09-902-540-13296	Sequence 13296, A
769	50.5	11.0	442	2	US-09-538-092-637	Sequence 637, App
770	50.5	11.0	455	2	US-09-543-681A-7043	Sequence 7043, Ap
771	50.5	11.0	461	2	US-09-107-532A-5964	Sequence 5964, Ap
772	50.5	11.0	467	2	US-09-902-540-11298	Sequence 11298, A
773	50.5	11.0	476	2	US-10-142-835-28	Sequence 28, Appl
774	50.5	11.0	477	2	US-09-252-991A-29825	Sequence 29825, A
775	50.5	11.0	499	2	US-09-252-991A-27221	Sequence 27221, A
776	50.5	11.0	529	1	US-07-891-942G-8	Sequence 8, Appli
777	50.5	11.0	529	1	US-08-370-909-19	Sequence 19, Appl
778	50.5	11.0	529	1	US-08-504-048-8	Sequence 8, Appli
779	50.5	11.0	529	2	US-09-341-982-1	Sequence 1, Appli
780	50.5	11.0	529	2	US-09-169-717E-39	Sequence 39, Appl
781	50.5	11.0	529	2	US-10-011-436-4	Sequence 4, Appli
782	50.5	11.0	529	2	US-08-533-895A-39	Sequence 39, Appl
783	50.5	11.0	537	2	US-08-540-922D-12	Sequence 12, Appl
784	50.5	11.0	550	1	US-08-279-700-18	Sequence 18, Appl
785	50.5	11.0	550	1	US-08-279-700-20	Sequence 20, Appl
786	50.5	11.0	550	1	US-08-279-700-22	Sequence 22, Appl
787	50.5	11.0	560	1	US-07-891-942G-5	Sequence 5, Appli
788	50.5	11.0	566	2	US-09-491-522-7	Sequence 7, Appli
789	50.5	11.0	566	2	US-09-949-016-7010	Sequence 7010, Ap
790	50.5	11.0	566	2	US-09-949-016-8505	Sequence 8505, Ap
791	50.5	11.0	566	2	US-09-949-002-452	Sequence 452, App
792	50.5	11.0	596	2	US-09-252-991A-22689	Sequence 22689, A
793	50.5	11.0	614	2	US-09-949-016-10772	Sequence 10772, A
794	50.5	11.0	757	2	US-09-902-540-11380	Sequence 11380, A
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796	50.5	11.0	974	2	US-08-938-291A-4	Sequence 4, Appli
797	50.5	11.0	974	2	US-09-589-619-4	Sequence 4, Appli
798	50.5	11.0	1106	2	US-09-134-000C-6136	Sequence 6136, Ap
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800	50.5	11.0	1163	1	US-08-286-889-4	Sequence 4, Appli
801	50.5	11.0	1163	1	US-08-485-618-4	Sequence 4, Appli
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803	50.5	11.0	1163	1	US-08-605-672-4	Sequence 4, Appli
804	50.5	11.0	1163	1	US-08-482-293A-4	Sequence 4, Appli
805	50.5	11.0	1163	1	US-08-943-363-4	Sequence 4, Appli
806	50.5	11.0	1163	1	US-08-476-062A-44	Sequence 44, Appl
807	50.5	11.0	1163	2	US-09-193-043-4	Sequence 4, Appli
808	50.5	11.0	1163	2	US-09-688-307A-4	Sequence 4, Appli
809	50.5	11.0	1163	2	US-09-350-259-4	Sequence 4, Appli
810	50.5	11.0	1163	4	PCT-US96-01314-44	Sequence 44, Appl
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812	50.5	11.0	1211	2	US-09-949-016-11401	Sequence 11401, A
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814	50.5	11.0	1211	2	US-09-949-002-555	Sequence 555, App
815	50.5	11.0	1245	2	US-09-252-991A-30935	Sequence 30935, A
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817	50.5	11.0	2703	1	US-08-185-432-19	Sequence 19, Appl
818	50.5	11.0	2703	2	US-08-899-232-4	Sequence 4, Appli
819	50.5	11.0	2703	2	US-09-121-457-4	Sequence 4, Appli
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821	50	10.8	31	2	US-09-270-767-37409	Sequence 37409, A
822	50	10.8	31	2	US-09-270-767-52626	Sequence 52626, A
823	50	10.8	69	2	US-09-248-796A-27038	Sequence 27038, A
824	50	10.8	92	2	US-09-127-946-8	Sequence 8, Appli
825	50	10.8	92	2	US-10-191-732-8	Sequence 8, Appli
826	50	10.8	93	2	US-09-148-545-256	Sequence 256, App
827	50	10.8	93	2	US-09-621-011-256	Sequence 256, App
828	50	10.8	102	2	US-09-198-452A-475	Sequence 475, App
829	50	10.8	105	2	US-09-248-796A-19711	Sequence 19711, A
830	50	10.8	119	2	US-09-482-273-264	Sequence 264, App

831	50	10.8	147	2	US-09-902-540-12970	Sequence 12970, A
832	50	10.8	195	2	US-09-394-142B-16	Sequence 16, Appl
833	50	10.8	201	2	US-09-270-767-31650	Sequence 31650, A
834	50	10.8	201	2	US-09-270-767-46867	Sequence 46867, A
835	50	10.8	248	2	US-09-634-238-279	Sequence 279, App
836	50	10.8	252	2	US-09-902-540-12546	Sequence 12546, A
837	50	10.8	261	2	US-09-543-681A-5280	Sequence 5280, Ap
838	50	10.8	263	2	US-09-328-352-4486	Sequence 4486, Ap
839	50	10.8	264	2	US-09-198-452A-266	Sequence 266, App
840	50	10.8	267	2	US-09-134-000C-6206	Sequence 6206, Ap
841	50	10.8	273	2	US-09-489-039A-12374	Sequence 12374, A
842	50	10.8	277	2	US-09-303-518D-400	Sequence 400, App
843	50	10.8	279	2	US-09-134-001C-4878	Sequence 4878, Ap
844	50	10.8	303	2	US-09-543-681A-5154	Sequence 5154, Ap
845	50	10.8	308	1	US-08-164-292B-18	Sequence 18, Appl
846	50	10.8	308	2	US-08-845-623-18	Sequence 18, Appl
847	50	10.8	308	2	US-08-815-927-18	Sequence 18, Appl
848	50	10.8	308	2	US-09-103-330-18	Sequence 18, Appl
849	50	10.8	308	2	US-09-435-242-18	Sequence 18, Appl
850	50	10.8	322	2	US-09-252-991A-24657	Sequence 24657, A
851	50	10.8	323	2	US-09-107-532A-6263	Sequence 6263, Ap
852	50	10.8	326	2	US-09-784-810C-11	Sequence 11, Appl
853	50	10.8	356	2	US-09-125-619-2	Sequence 2, Appli
854	50	10.8	356	2	US-09-125-619-13	Sequence 13, Appl
855	50	10.8	356	2	US-10-222-566-2	Sequence 2, Appli
856	50	10.8	356	2	US-10-222-566-13	Sequence 13, Appl
857	50	10.8	356	2	US-10-143-024A-2	Sequence 2, Appli
858	50	10.8	356	2	US-10-143-024A-13	Sequence 13, Appl
859	50	10.8	356	2	US-10-222-162-2	Sequence 2, Appli
860	50	10.8	356	2	US-10-222-162-13	Sequence 13, Appl
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862	50	10.8	378	2	US-09-902-540-11860	Sequence 11860, A
863	50	10.8	390	2	US-09-710-279-1422	Sequence 1422, Ap
864	50	10.8	427	2	US-09-902-540-15413	Sequence 15413, A
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868	50	10.8	461	2	US-09-543-681A-6448	Sequence 6448, Ap
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870	50	10.8	471	2	US-09-784-810C-6	Sequence 6, Appli
871	50	10.8	501	2	US-09-252-991A-31885	Sequence 31885, A
872	50	10.8	521	2	US-09-134-001C-4290	Sequence 4290, Ap
873	50	10.8	525	2	US-09-949-016-7407	Sequence 7407, Ap
874	50	10.8	533	2	US-09-549-519-31	Sequence 31, Appl
875	50	10.8	544	2	US-09-252-991A-26096	Sequence 26096, A
876	50	10.8	605	2	US-09-949-016-8269	Sequence 8269, Ap
877	50	10.8	606	2	US-09-538-092-798	Sequence 798, App
878	50	10.8	641	2	US-09-653-274-13	Sequence 13, Appl
879	50	10.8	641	2	US-10-461-791-13	Sequence 13, Appl
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882	50	10.8	1070	2	US-10-461-791-8	Sequence 8, Appli
883	50	10.8	1086	2	US-09-653-274-4	Sequence 4, Appli
884	50	10.8	1086	2	US-10-461-791-4	Sequence 4, Appli
885	50	10.8	1309	2	US-09-862-027-82	Sequence 82, Appl
886	50	10.8	1381	2	US-08-826-134-4	Sequence 4, Appli
887	50	10.8	1443	1	US-08-308-872B-2	Sequence 2, Appli
888	50	10.8	1479	2	US-08-840-062-2	Sequence 2, Appli
889	49.5	10.7	58	1	US-08-721-746-2	Sequence 2, Appli
890	49.5	10.7	59	2	US-09-513-999C-6346	Sequence 6346, Ap
891	49.5	10.7	66	2	US-09-513-999C-7224	Sequence 7224, Ap
892	49.5	10.7	160	2	US-09-732-210-304	Sequence 304, App
893	49.5	10.7	160	2	US-09-107-532A-5111	Sequence 5111, Ap
894	49.5	10.7	172	2	US-08-772-270A-1	Sequence 1, Appli
895	49.5	10.7	172	2	US-09-062-126-2	Sequence 2, Appli
896	49.5	10.7	193	2	US-09-475-316A-78	Sequence 78, Appl
897	49.5	10.7	193	2	US-09-704-640-78	Sequence 78, Appl
898	49.5	10.7	200	1	US-08-698-805-6	Sequence 6, Appli
899	49.5	10.7	212	2	US-09-813-453B-59	Sequence 59, Appl
900	49.5	10.7	246	2	US-09-134-001C-5292	Sequence 5292, Ap
901	49.5	10.7	249	1	US-08-626-685A-11	Sequence 11, Appl
902	49.5	10.7	249	2	US-09-248-796A-19210	Sequence 19210, A
903	49.5	10.7	252	1	US-07-885-089B-7	Sequence 7, Appli
904	49.5	10.7	252	2	US-09-976-594-582	Sequence 582, App
905	49.5	10.7	252	2	US-09-919-039-228	Sequence 228, App
906	49.5	10.7	262	2	US-09-134-001C-3746	Sequence 3746, Ap
907	49.5	10.7	262	2	US-09-710-279-1568	Sequence 1568, Ap
908	49.5	10.7	265	2	US-09-780-016-8	Sequence 8, Appli
909	49.5	10.7	265	2	US-10-214-811-8	Sequence 8, Appli
910	49.5	10.7	265	2	US-10-766-074-8	Sequence 8, Appli
911	49.5	10.7	268	2	US-09-716-964B-156	Sequence 156, App
912	49.5	10.7	290	2	US-09-780-016-6	Sequence 6, Appli
913	49.5	10.7	290	2	US-10-214-811-6	Sequence 6, Appli
914	49.5	10.7	290	2	US-10-766-074-6	Sequence 6, Appli
915	49.5	10.7	296	2	US-09-489-847-293	Sequence 293, App
916	49.5	10.7	315	2	US-09-107-532A-5917	Sequence 5917, Ap
917	49.5	10.7	319	2	US-09-252-991A-28066	Sequence 28066, A
918	49.5	10.7	320	2	US-09-489-039A-10349	Sequence 10349, A
919	49.5	10.7	322	2	US-09-949-016-11381	Sequence 11381, A
920	49.5	10.7	324	2	US-09-602-787A-484	Sequence 484, App
921	49.5	10.7	328	2	US-09-605-703B-2840	Sequence 2840, Ap
922	49.5	10.7	353	2	US-09-489-039A-12270	Sequence 12270, A
923	49.5	10.7	363	2	US-09-949-016-11040	Sequence 11040, A
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926	49.5	10.7	372	2	US-08-993-088A-2	Sequence 2, Appli
927	49.5	10.7	372	2	US-08-993-088A-20	Sequence 20, Appl
928	49.5	10.7	372	2	US-08-993-424B-2	Sequence 2, Appli
929	49.5	10.7	372	2	US-08-665-034A-2	Sequence 2, Appli
930	49.5	10.7	372	2	US-08-665-034A-4	Sequence 4, Appli
931	49.5	10.7	372	2	US-09-595-549-9	Sequence 9, Appli
932	49.5	10.7	372	2	US-09-603-680-2	Sequence 2, Appli
933	49.5	10.7	372	2	US-09-603-680-20	Sequence 20, Appl
934	49.5	10.7	372	2	US-08-981-700A-2	Sequence 2, Appli
935	49.5	10.7	372	2	US-08-899-112B-8	Sequence 8, Appli
936	49.5	10.7	372	2	US-09-011-553-2	Sequence 2, Appli
937	49.5	10.7	378	2	US-09-689-486-62	Sequence 62, Appl
938	49.5	10.7	380	2	US-09-120-365-76	Sequence 76, Appl
939	49.5	10.7	380	2	US-09-515-039-76	Sequence 76, Appl
940	49.5	10.7	380	2	US-08-860-255A-5	Sequence 5, Appli
941	49.5	10.7	394	2	US-09-710-279-3292	Sequence 3292, Ap
942	49.5	10.7	403	2	US-09-489-039A-11022	Sequence 11022, A
943	49.5	10.7	414	2	US-09-710-279-806	Sequence 806, App
944	49.5	10.7	420	2	US-09-252-991A-30428	Sequence 30428, A
945	49.5	10.7	423	2	US-09-134-001C-3599	Sequence 3599, Ap
946	49.5	10.7	427	2	US-09-328-352-6602	Sequence 6602, Ap
947	49.5	10.7	436	2	US-09-902-540-9717	Sequence 9717, Ap
948	49.5	10.7	462	2	US-09-886-319A-72	Sequence 72, Appl
949	49.5	10.7	469	2	US-08-753-007A-8	Sequence 8, Appli
950	49.5	10.7	469	2	US-09-398-496-8	Sequence 8, Appli
951	49.5	10.7	470	2	US-10-104-047-3775	Sequence 3775, Ap
952	49.5	10.7	476	2	US-09-134-001C-3778	Sequence 3778, Ap
953	49.5	10.7	498	2	US-09-248-796A-15018	Sequence 15018, A
954	49.5	10.7	507	2	US-09-780-016-2	Sequence 2, Appli
955	49.5	10.7	507	2	US-10-214-811-2	Sequence 2, Appli
956	49.5	10.7	507	2	US-10-766-074-2	Sequence 2, Appli
957	49.5	10.7	532	2	US-09-780-016-20	Sequence 20, Appl
958	49.5	10.7	532	2	US-10-214-811-20	Sequence 20, Appl
959	49.5	10.7	532	2	US-10-766-074-20	Sequence 20, Appl
960	49.5	10.7	556	2	US-09-907-794A-259	Sequence 259, App
961	49.5	10.7	556	2	US-09-905-125A-259	Sequence 259, App
962	49.5	10.7	556	2	US-09-902-775A-259	Sequence 259, App
963	49.5	10.7	556	2	US-09-906-700-259	Sequence 259, App
964	49.5	10.7	556	2	US-09-903-603A-259	Sequence 259, App
965	49.5	10.7	556	2	US-09-904-920A-259	Sequence 259, App
966	49.5	10.7	556	2	US-09-909-064-259	Sequence 259, App
967	49.5	10.7	556	2	US-09-905-381A-259	Sequence 259, App
968	49.5	10.7	556	2	US-09-906-618-259	Sequence 259, App
969	49.5	10.7	556	2	US-09-906-646-259	Sequence 259, App
970	49.5	10.7	556	2	US-09-904-462-259	Sequence 259, App
971	49.5	10.7	556	2	US-09-902-736A-259	Sequence 259, App
972	49.5	10.7	556	2	US-09-906-722A-259	Sequence 259, App
973	49.5	10.7	557	2	US-10-771-708-4	Sequence 4, Appli
974	49.5	10.7	563	2	US-08-931-608A-3	Sequence 3, Appli
975	49.5	10.7	563	2	US-09-851-847-3	Sequence 3, Appli
976	49.5	10.7	582	2	US-09-252-991A-21510	Sequence 21510, A

977	49.5	10.7	597	2	US-09-252-991A-32657	Sequence 32657, A
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979	49.5	10.7	637	2	US-09-569-611C-35	Sequence 35, Appl
980	49.5	10.7	647	2	US-08-753-007A-32	Sequence 32, Appl
981	49.5	10.7	647	2	US-09-398-496-32	Sequence 32, Appl
982	49.5	10.7	660	2	US-09-907-794A-28	Sequence 28, Appl
983	49.5	10.7	660	2	US-09-905-125A-28	Sequence 28, Appl
984	49.5	10.7	660	2	US-09-902-775A-28	Sequence 28, Appl
985	49.5	10.7	660	2	US-09-906-700-28	Sequence 28, Appl
986	49.5	10.7	660	2	US-09-903-603A-28	Sequence 28, Appl
987	49.5	10.7	660	2	US-09-904-920A-28	Sequence 28, Appl
988	49.5	10.7	660	2	US-09-949-016-6843	Sequence 6843, Ap
989	49.5	10.7	660	2	US-09-909-064-28	Sequence 28, Appl
990	49.5	10.7	660	2	US-09-905-381A-28	Sequence 28, Appl
991	49.5	10.7	660	2	US-09-906-618-28	Sequence 28, Appl
992	49.5	10.7	660	2	US-09-906-646-28	Sequence 28, Appl
993	49.5	10.7	660	2	US-09-689-486-58	Sequence 58, Appl
994	49.5	10.7	660	2	US-09-904-462-28	Sequence 28, Appl
995	49.5	10.7	660	2	US-09-902-736A-28	Sequence 28, Appl
996	49.5	10.7	660	2	US-09-906-722A-28	Sequence 28, Appl
997	49.5	10.7	661	2	US-09-252-991A-27070	Sequence 27070, A
998	49.5	10.7	662	2	US-09-902-540-12594	Sequence 12594, A
999	49.5	10.7	683	2	US-09-949-016-7267	Sequence 7267, Ap
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1005	49	10.6	70	2	US-09-248-796A-23329	Sequence 23329, A
1006	49	10.6	103	2	US-09-543-681A-7951	Sequence 7951, Ap
1007	49	10.6	118	2	US-09-056-556-231	Sequence 231, App
1008	49	10.6	118	2	US-09-072-596-226	Sequence 226, App
1009	49	10.6	118	2	US-09-072-967-231	Sequence 231, App
1010	49	10.6	118	2	US-10-193-002-226	Sequence 226, App
1011	49	10.6	118	2	US-10-084-843-231	Sequence 231, App
1012	49	10.6	156	2	US-09-134-001C-4234	Sequence 4234, Ap
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1015	49	10.6	190	2	US-09-704-640-29	Sequence 29, Appl
1016	49	10.6	190	2	US-09-704-640-31	Sequence 31, Appl
1017	49	10.6	195	1	US-08-403-852D-24	Sequence 24, Appl
1018	49	10.6	195	2	US-08-510-646B-25	Sequence 25, Appl
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1025	49	10.6	219	2	US-10-115-123-151	Sequence 151, App
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1029	49	10.6	235	2	US-09-902-540-15987	Sequence 15987, A
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1035	49	10.6	262	2	US-09-956-086-4	Sequence 4, Appli
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ALIGNMENTS

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RESULT 1
US-09-289-349-11
; Sequence 11, Application US/09289349
; Patent No. 6277574
; GENERAL INFORMATION:
;  APPLICANT: Walker, Michael, G.
;  APPLICANT: Volkmuth, Wayne
;  APPLICANT: Klinger, Tod, M.
;  APPLICANT: Azimzai, Yalda
;  APPLICANT: Yue, Henry
;  TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY
;  FILE REFERENCE: PB-0010 US
;  CURRENT APPLICATION NUMBER: US/09/289,349
;  CURRENT FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PERL Program
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;   FEATURE: -
;   OTHER INFORMATION: 1900433CD1
US-09-289-349-11

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RESULT 2
US-09-991-181-262
; Sequence 262, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
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; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
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Query Match 100.0%; Score 461; DB 2; Length 89;
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RESULT 3
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 461; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2e-51;
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RESULT 4
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; Sequence 262, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
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; APPLICANT: Eaton,Dan L.
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
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; PRIOR FILING DATE: 1998-06-25

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; PRIOR APPLICATION NUMBER: 60/090695
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 461; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60
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Db          1 MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60

Qy         61 CKYKSSQKQHSPVPEKAIPLITPGSATTC 89
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Db         61 CKYKSSQKQHSPVPEKAIPLITPGSATTC 89
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RESULT 5
US-09-992-598-262
; Sequence 262, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/088858
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; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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  Query Match             100.0%;  Score 461;  DB 2;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 2e-51;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60
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Db          1 MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60

Qy         61 CKYKSSQKQHSPVPEKAIPLITPGSATTC 89
              |||||||||||||||||||||||||||||
Db         61 CKYKSSQKQHSPVPEKAIPLITPGSATTC 89
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RESULT 6
US-09-724-864-58
; Sequence 58, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-58

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  Best Local Similarity   66.7%;  Pred. No. 9e-28;
  Matches   60;  Conservative    8;  Mismatches   19;  Indels    3;  Gaps    3;

Qy          1 MERVTLA-LLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
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Db          1 MEEITCAFLLLLAGLPALEASDP-VDKDSPFYYDWESLQLGGLIFGGLLCIAGIAMALSG 59
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Qy          60 KCKYKSSQKQHSPVPEKAIPLITPGSATTC 89
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Db          60 KCKCRRTHKP-SSLPGKATPLIIPGSANTC 88


RESULT 7
US-08-725-531-5
; Sequence 5, Application US/08725531
; Patent No. 5756310
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Goli, Surya K.
;    TITLE OF INVENTION:  NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/725,531
;      FILING DATE:  Filed Herewith
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0128 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  951423
US-08-725-531-5

  Query Match             55.6%;  Score 256.5;  DB 1;  Length 87;
  Best Local Similarity   61.5%;  Pred. No. 3.2e-25;
  Matches   56;  Conservative   11;  Mismatches   17;  Indels    7;  Gaps    4;

Qy           1 MERVTLA-LLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
               || :| | ||:|||| |||| |  :|  ||||||::||| |:| |||| |||||  |||
Db           1 MEGITCAFLLVLAGLPVLEANGP-VDKGSPFYYDWESLQLGGMIFGGLLCIAGIAMALSG 59

Qy          60 KCKYKSSQKQHSP--VPEKAIPLITPGSATT 88
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Db          60 KCK---CRRNHTPSSLPEKVTPLITPGSAST 87


RESULT 8
US-08-738-127-5
; Sequence 5, Application US/08738127
; Patent No. 5919655
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Hawkins, Phillip R.
;    TITLE OF INVENTION:  NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/738,127
;      FILING DATE:  Filed Herewith
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0141 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  951423
US-08-738-127-5

  Query Match             55.6%;  Score 256.5;  DB 1;  Length 87;
  Best Local Similarity   61.5%;  Pred. No. 3.2e-25;
  Matches   56;  Conservative   11;  Mismatches   17;  Indels    7;  Gaps    4;

Qy           1 MERVTLA-LLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
               || :| | ||:|||| |||| |  :|  ||||||::||| |:| |||| |||||  |||
Db           1 MEGITCAFLLVLAGLPVLEANGP-VDKGSPFYYDWESLQLGGMIFGGLLCIAGIAMALSG 59

Qy          60 KCKYKSSQKQHSP--VPEKAIPLITPGSATT 88
               |||    :: |:|  :|||  ||||||||:|
Db          60 KCK---CRRNHTPSSLPEKVTPLITPGSAST 87


RESULT 9
US-09-213-392-5
; Sequence 5, Application US/09213392
; Patent No. 5945505
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Goli, Surya K.
;    TITLE OF INVENTION:  NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/213,392
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;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  09/083,661
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J.
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0128 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  87 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:  GenBank
;       CLONE:  951423
US-09-213-392-5

  Query Match             55.6%;  Score 256.5;  DB 1;  Length 87;
  Best Local Similarity   61.5%;  Pred. No. 3.2e-25;
  Matches   56;  Conservative   11;  Mismatches   17;  Indels    7;  Gaps    4;

Qy          1 MERVTLA-LLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              || :| | ||:|||| |||| |  :|  ||||||::||| |:| |||| |||||  |||
Db          1 MEGITCAFLLVLAGLPVLEANGP-VDKGSPFYYDWESLQLGGMIFGGLLCIAGIAMALSG 59

Qy         60 KCKYKSSQKQHSP--VPEKAIPLITPGSATT 88
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Db         60 KCK---CRRNHTPSSLPEKVTPLITPGSAST 87


RESULT 10
US-09-083-661-5
; Sequence 5, Application US/09083661
; Patent No. 5955283
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Goli, Surya K.
;    TITLE OF INVENTION:  NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/083,661
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,531
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0128 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  951423
US-09-083-661-5

  Query Match             55.6%;  Score 256.5;  DB 1;  Length 87;
  Best Local Similarity   61.5%;  Pred. No. 3.2e-25;
  Matches   56;  Conservative   11;  Mismatches   17;  Indels    7;  Gaps    4;

Qy          1 MERVTLA-LLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              || :| | ||:|||| |||| |  :|  ||||||::||| |:| |||| |||||  |||
Db          1 MEGITCAFLLVLAGLPVLEANGP-VDKGSPFYYDWESLQLGGMIFGGLLCIAGIAMALSG 59

Qy         60 KCKYKSSQKQHSP--VPEKAIPLITPGSATT 88
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Db         60 KCK---CRRNHTPSSLPEKVTPLITPGSAST 87


RESULT 11
US-08-289-247B-4
; Sequence 4, Application US/08289247B
; Patent No. 5728579
;  GENERAL INFORMATION:
;    APPLICANT:  Morrison, Briggs W.
;    APPLICANT:  Leder, Philip
;    TITLE OF INVENTION:  Detection and Treatment of Breast
;    TITLE OF INVENTION:  Cancer
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2223
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/289,247B
;      FILING DATE:  August 11, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bieker-Brady, Kristina
;      REGISTRATION NUMBER:  39,109
;      REFERENCE/DOCKET NUMBER:  00383/021001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 428-0200
;      TELEFAX:  (617) 428-7045
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-289-247B-4

  Query Match             46.5%;  Score 214.5;  DB 1;  Length 87;
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Qy          1 MERVTLALLL-LAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
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Db          1 MQKVTLGLLVFLAGFPVLDAND-LEDKNSPFYYDWHSLQVGGLICAGVLCAMGIIIVMSA 59
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Qy          60 KCKYKSSQKQ-HSPVPEKAIPLITPGSA 86
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Db          60 KCKCKFGQKSGHH--PGETPPLITPGSA 85


RESULT 12
US-08-725-531-4
; Sequence 4, Application US/08725531
; Patent No. 5756310
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Goli, Surya K.
;    TITLE OF INVENTION:  NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/725,531
;      FILING DATE:  Filed Herewith
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0128 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  1085026
US-08-725-531-4

  Query Match             46.5%;  Score 214.5;  DB 1;  Length 87;
  Best Local Similarity   54.5%;  Pred. No. 7.9e-20;
  Matches   48;  Conservative   11;  Mismatches   24;  Indels    5;  Gaps    4;

Qy           1 MERVTLALLL-LAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
               |::||| ||: ||| . |:|||   :|: |||||| :||: |||| |:|   ||  |:|
Db           1 MQKVTLGLLVFLAGFPVLDAND-LEDKNSPFYYDWHSLQVGGLICAGVLCAMGIIIVMSA 59

Qy          60 KCKYKSSQKQ-HSPVPEKAIPLITPGSA 86
               ||| |  ||  |   | :  ||||||||
Db          60 KCKCKFGQKSGHH--PGETPPLITPGSA 85


RESULT 13
US-08-738-127-4
; Sequence 4, Application US/08738127
; Patent No. 5919655
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Hawkins, Phillip R.
;    TITLE OF INVENTION:  NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/738,127
;      FILING DATE:  Filed Herewith
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0141 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  1085026
US-08-738-127-4

  Query Match             46.5%;  Score 214.5;  DB 1;  Length 87;
  Best Local Similarity   54.5%;  Pred. No. 7.9e-20;
  Matches   48;  Conservative   11;  Mismatches   24;  Indels    5;  Gaps    4;

Qy           1 MERVTLALLL-LAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
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Db           1 MQKVTLGLLVFLAGFPVLDAND-LEDKNSPFYYDWHSLQVGGLICAGVLCAMGIIIVMSA 59

Qy          60 KCKYKSSQKQ-HSPVPEKAIPLITPGSA 86
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Db          60 KCKCKFGQKSGHH--PGETPPLITPGSA 85


RESULT 14
US-09-213-392-4
; Sequence 4, Application US/09213392
; Patent No. 5945505
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Goli, Surya K.
;    TITLE OF INVENTION:  NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/09/213,392
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/083,661
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0128 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  1085026
US-09-213-392-4

  Query Match           46.5%;  Score 214.5;  DB 1;  Length 87;
  Best Local Similarity  54.5%;  Pred. No. 7.9e-20;
  Matches   48;  Conservative   11;  Mismatches   24;  Indels    5;  Gaps    4;

Qy          1 MERVTLALLL-LAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              |::||| ||: ||| |:||| :|: |||||| :||: |||| |:|  || |:|
Db          1 MQKVTLGLLVFLAGFPVLDAND-LEDKNSPFYYDWHSLQVGGLICAGVLCAMGIIIVMSA 59

Qy         60 KCKYKSSQKQ-HSPVPEKAIPLITPGSA 86
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Db         60 KCKCKFGQKSGHH--PGETPPLITPGSA 85


RESULT 15
US-09-083-661-4
; Sequence 4, Application US/09083661
; Patent No. 5955283
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Goli, Surya K.
;    TITLE OF INVENTION:  NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/083,661
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,531
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0128 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  1085026
US-09-083-661-4

  Query Match           46.5%;  Score 214.5;  DB 1;  Length 87;
  Best Local Similarity  54.5%;  Pred. No. 7.9e-20;
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Qy          1 MERVTLALLL-LAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
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Db          1 MQKVTLGLLVFLAGFPVLDAND-LEDKNSPFYYDWHSLQVGGLICAGVLCAMGIIIVMSA 59

Qy         60 KCKYKSSQKQ-HSPVPEKAIPLITPGSA 86
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Db         60 KCKCKFGQKSGHH--PGETPPLITPGSA 85


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Job time : 69 secs
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GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 12, 2006, 21:40:45 ; Search time 165 Seconds
(without alignments)
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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
27	461	100.0	89	3	US-09-997-428-262	Sequence 262, App
562	461	100.0	89	4	US-10-174-587-200	Sequence 200, App
626	461	100.0	89	4	US-10-063-742-50	Sequence 50, Appl
741	461	100.0	89	5	US-10-972-317-50	Sequence 50, Appl
742	461	100.0	89	5	US-10-820-474A-35	Sequence 35, Appl
744	461	100.0	89	5	US-10-950-374-262	Sequence 262, App
747	374	81.1	186	4	US-10-295-027-210	Sequence 210, App
748	374	81.1	318	4	US-10-295-027-212	Sequence 212, App
749	276.5	60.0	88	3	US-09-866-050A-698	Sequence 698, App
750	214.5	46.5	87	4	US-10-176-847-24	Sequence 24, Appl
751	214.5	46.5	87	4	US-10-205-823-140	Sequence 140, App
752	214.5	46.5	87	4	US-10-177-293-166	Sequence 166, App
753	214.5	46.5	87	4	US-10-295-027-1358	Sequence 1358, Ap
754	214.5	46.5	87	6	US-11-051-454-140	Sequence 140, App
755	214.5	46.5	116	4	US-10-161-493-34	Sequence 34, Appl
756	209.5	45.4	86	4	US-10-161-493-32	Sequence 32, Appl
757	191.5	41.5	113	4	US-10-205-823-142	Sequence 142, App
758	191.5	41.5	113	4	US-10-177-293-168	Sequence 168, App
759	191.5	41.5	113	4	US-10-295-027-1357	Sequence 1357, Ap
760	191.5	41.5	113	6	US-11-051-454-142	Sequence 142, App
761	191.5	41.5	150	3	US-09-925-299-955	Sequence 955, App
762	191.5	41.5	150	3	US-09-925-299-955	Sequence 955, App
763	129	28.0	92	3	US-09-981-876-238	Sequence 238, App
764	129	28.0	92	3	US-09-148-545-238	Sequence 238, App
765	129	28.0	92	3	US-09-903-190-120	Sequence 120, App
766	129	28.0	92	3	US-09-978-360A-776	Sequence 776, App
767	129	28.0	92	4	US-10-408-765A-1270	Sequence 1270, Ap
768	129	28.0	92	5	US-10-930-331-120	Sequence 120, App
769	129	28.0	92	5	US-10-979-111-238	Sequence 238, App
770	129	28.0	93	3	US-09-981-876-183	Sequence 183, App
771	129	28.0	93	3	US-09-148-545-183	Sequence 183, App
772	129	28.0	93	5	US-10-979-111-183	Sequence 183, App
773	121	26.2	70	3	US-09-981-876-269	Sequence 269, App
774	121	26.2	70	3	US-09-148-545-269	Sequence 269, App
775	121	26.2	70	5	US-10-979-111-269	Sequence 269, App
776	113.5	24.6	138	4	US-10-291-265-446	Sequence 446, App
777	112.5	24.4	95	4	US-10-291-265-918	Sequence 918, App
778	112.5	24.4	96	3	US-09-809-391-473	Sequence 473, App
779	112.5	24.4	96	3	US-09-882-171-473	Sequence 473, App
780	112.5	24.4	96	4	US-10-164-861-473	Sequence 473, App
807	112.5	24.4	120	3	US-09-997-428-199	Sequence 199, App
1296	112.5	24.4	120	5	US-10-931-886-434	Sequence 434, App
1298	112.5	24.4	120	5	US-10-955-952-434	Sequence 434, App
1299	112.5	24.4	120	5	US-10-950-374-199	Sequence 199, App
1300	106	23.0	69	3	US-09-809-391-606	Sequence 606, App
1301	106	23.0	69	3	US-09-882-171-606	Sequence 606, App
1302	106	23.0	69	4	US-10-164-861-606	Sequence 606, App
1303	105.5	22.9	110	5	US-10-450-763-56705	Sequence 56705, A
1304	94	20.4	115	4	US-10-352-272-2	Sequence 2, Appli
1305	94	20.4	178	3	US-09-833-245-1532	Sequence 1532, Ap
1306	94	20.4	178	3	US-09-985-153-92	Sequence 92, Appl
1307	94	20.4	178	3	US-09-985-153-93	Sequence 93, Appl
1308	94	20.4	178	3	US-09-985-153-94	Sequence 94, Appl
1309	94	20.4	178	3	US-09-985-153-96	Sequence 96, Appl

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Job time : 166 secs

GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 12, 2006, 21:41:45 ; Search time 28 Seconds
(without alignments)
149.230 Million cell updates/sec

Perfect score: 461
Sequence: 1 MERVTLALLLLAGLTALEAN.....HSPVPEKAIPLITPGSATTC 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published_Applications_AA_New:*
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5: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
7	461	100.0	89	11	US-11-102-240-50	Sequence 50, Appl
8	461	100.0	89	11	US-11-103-195-50	Sequence 50, Appl
9	447	97.0	89	9	US-10-986-405-330	Sequence 330, App
10	214.5	46.5	87	9	US-10-821-234-1279	Sequence 1279, Ap
11	214.5	46.5	87	9	US-10-475-075-192	Sequence 192, App
12	214.5	46.5	87	9	US-10-475-075-476	Sequence 476, App
13	214.5	46.5	87	11	US-11-080-991-24	Sequence 24, Appl
14	129	28.0	92	7	US-09-978-360A-776	Sequence 776, App
15	113.5	24.6	138	11	US-11-000-463-446	Sequence 446, App
16	112.5	24.4	95	11	US-11-000-463-918	Sequence 918, App
17	112.5	24.4	96	11	US-11-144-947-473	Sequence 473, App
19	112.5	24.4	120	9	US-10-973-115B-434	Sequence 434, App
22	112.5	24.4	120	11	US-11-290-153-434	Sequence 434, App
23	106	23.0	69	11	US-11-144-947-606	Sequence 606, App
25	94	20.4	178	9	US-10-821-234-1495	Sequence 1495, Ap
30	94	20.4	178	11	US-11-152-366-46	Sequence 46, Appl
31	94	20.4	178	11	US-11-072-175-173	Sequence 173, App
32	94	20.4	178	11	US-11-264-096-1532	Sequence 1532, Ap
33	94	20.4	219	11	US-11-264-096-1531	Sequence 1531, Ap
34	89	19.3	80	9	US-10-475-075-276	Sequence 276, App
35	89	19.3	80	9	US-10-475-075-534	Sequence 534, App
36	67.5	14.6	664	11	US-11-080-991-40	Sequence 40, Appl
37	66.5	14.4	523	11	US-11-288-493-10	Sequence 10, Appl
38	63.5	13.8	286	11	US-11-098-686-11112	Sequence 11112, A
39	63.5	13.8	309	11	US-11-045-004-1223	Sequence 1223, Ap
60	62.5	13.6	339	11	US-11-226-657-66	Sequence 66, Appl
61	62.5	13.6	340	11	US-11-226-657-174	Sequence 174, App
62	62	13.4	599	9	US-10-455-772-110	Sequence 110, App
63	62	13.4	605	9	US-10-455-772-106	Sequence 106, App
64	62	13.4	613	9	US-10-455-772-112	Sequence 112, App
65	62	13.4	638	9	US-10-455-772-104	Sequence 104, App
66	61.5	13.3	977	11	US-11-093-274-39	Sequence 39, Appl
67	61.5	13.3	1145	11	US-11-188-298-16637	Sequence 16637, A
68	61	13.2	139	9	US-10-467-657-4932	Sequence 4932, Ap
69	60.5	13.1	106	11	US-11-144-947-341	Sequence 341, App
70	60.5	13.1	463	11	US-11-087-099-7201	Sequence 7201, Ap
71	60.5	13.1	463	11	US-11-087-099-11335	Sequence 11335, A
72	60.5	13.1	463	11	US-11-188-298-6612	Sequence 6612, Ap
73	60.5	13.1	463	11	US-11-188-298-21475	Sequence 21475, A
74	60	13.0	188	11	US-11-096-568A-23885	Sequence 23885, A
75	60	13.0	256	11	US-11-096-568A-23884	Sequence 23884, A
76	60	13.0	525	11	US-11-052-554A-209	Sequence 209, App
77	59	12.8	310	11	US-11-188-298-17559	Sequence 17559, A
78	59	12.8	544	11	US-11-201-916-6	Sequence 6, Appli
79	59	12.8	858	9	US-10-613-744-6	Sequence 6, Appli
80	58.5	12.7	164	9	US-10-510-321-1	Sequence 1, Appli
82	58.5	12.7	260	9	US-10-510-321-2	Sequence 2, Appli
83	58.5	12.7	260	9	US-10-973-115B-396	Sequence 396, App
87	58.5	12.7	260	11	US-11-251-455-7	Sequence 7, Appli
88	58.5	12.7	260	11	US-11-290-153-396	Sequence 396, App
89	58.5	12.7	336	11	US-11-188-298-10284	Sequence 10284, A
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91	58.5	12.7	383	11	US-11-202-731-32	Sequence 32, Appl
92	58.5	12.7	409	11	US-11-188-298-17265	Sequence 17265, A
93	58.5	12.7	565	11	US-11-188-298-12654	Sequence 12654, A
94	58.5	12.7	837	9	US-10-467-657-1464	Sequence 1464, Ap
95	58.5	12.7	1095	11	US-11-096-568A-29175	Sequence 29175, A
96	58.5	12.7	1118	11	US-11-096-568A-30471	Sequence 30471, A
97	58	12.6	366	11	US-11-096-568A-30916	Sequence 30916, A
98	58	12.6	394	11	US-11-188-298-926	Sequence 926, App
99	58	12.6	394	11	US-11-188-298-1319	Sequence 1319, Ap
100	58	12.6	394	11	US-11-188-298-15528	Sequence 15528, A
101	58	12.6	478	11	US-11-096-568A-30915	Sequence 30915, A
102	58	12.6	484	11	US-11-096-568A-30914	Sequence 30914, A
103	58	12.6	681	11	US-11-072-512-3586	Sequence 3586, Ap
104	57.5	12.5	264	11	US-11-096-568A-32530	Sequence 32530, A
105	57.5	12.5	324	9	US-10-858-730-113	Sequence 113, App
106	57.5	12.5	336	11	US-11-096-568A-32529	Sequence 32529, A
107	57.5	12.5	353	11	US-11-096-568A-32528	Sequence 32528, A
108	57.5	12.5	425	11	US-11-188-298-19226	Sequence 19226, A
109	57.5	12.5	2238	9	US-10-330-773-42	Sequence 42, Appl
110	57.5	12.5	2910	9	US-10-330-773-39	Sequence 39, Appl
111	57	12.4	457	11	US-11-087-099-2494	Sequence 2494, Ap
112	57	12.4	457	11	US-11-087-099-3478	Sequence 3478, Ap
113	57	12.4	457	11	US-11-188-298-2380	Sequence 2380, Ap
114	57	12.4	457	11	US-11-188-298-3280	Sequence 3280, Ap
115	57	12.4	458	11	US-11-087-099-9639	Sequence 9639, Ap
116	57	12.4	458	11	US-11-087-099-11216	Sequence 11216, A
117	57	12.4	458	11	US-11-188-298-8947	Sequence 8947, Ap
118	57	12.4	458	11	US-11-188-298-10343	Sequence 10343, A
119	56.5	12.3	148	9	US-10-512-109-19	Sequence 19, Appl
120	56.5	12.3	240	11	US-11-087-099-7357	Sequence 7357, Ap
121	56.5	12.3	260	11	US-11-183-914-7	Sequence 7, Appli
122	56.5	12.3	284	11	US-11-087-099-9686	Sequence 9686, Ap
123	56.5	12.3	408	11	US-11-188-298-19509	Sequence 19509, A
124	56.5	12.3	409	11	US-11-188-298-12135	Sequence 12135, A
125	56.5	12.3	595	9	US-10-537-002-45	Sequence 45, Appl
126	56.5	12.3	597	11	US-11-098-686-10197	Sequence 10197, A
127	56.5	12.3	670	11	US-11-188-298-15016	Sequence 15016, A
128	56.5	12.3	975	9	US-10-745-586-161	Sequence 161, App
129	56	12.1	209	11	US-11-079-463-9528	Sequence 9528, Ap
130	56	12.1	409	11	US-11-188-298-3216	Sequence 3216, Ap
131	56	12.1	434	11	US-11-188-298-9681	Sequence 9681, Ap
132	56	12.1	531	11	US-11-188-298-14335	Sequence 14335, A
133	56	12.1	736	11	US-11-087-099-8431	Sequence 8431, Ap

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136	55.5	12.0	222	9	US-10-993-143-15	Sequence 15, Appl
137	55.5	12.0	240	11	US-11-087-099-8864	Sequence 8864, Ap
138	55.5	12.0	384	11	US-11-108-185-14	Sequence 14, Appl
139	55.5	12.0	384	11	US-11-108-185-16	Sequence 16, Appl
140	55.5	12.0	384	11	US-11-108-185-18	Sequence 18, Appl
141	55.5	12.0	407	11	US-11-087-099-1880	Sequence 1880, Ap
142	55.5	12.0	459	11	US-11-087-099-7856	Sequence 7856, Ap
143	55.5	12.0	587	11	US-11-172-740-967	Sequence 967, App
145	55.5	12.0	888	9	US-10-973-115B-544	Sequence 544, App
149	55.5	12.0	888	11	US-11-290-153-544	Sequence 544, App
150	55.5	12.0	968	9	US-10-506-454-1177	Sequence 1177, Ap
151	55	11.9	255	9	US-10-506-454-1677	Sequence 1677, Ap
152	55	11.9	324	9	US-10-506-454-703	Sequence 703, App
153	55	11.9	433	11	US-11-087-099-8577	Sequence 8577, Ap
154	55	11.9	482	11	US-11-045-004-1364	Sequence 1364, Ap
155	55	11.9	604	11	US-11-188-298-20515	Sequence 20515, A
156	55	11.9	613	11	US-11-096-568A-29070	Sequence 29070, A
157	55	11.9	631	11	US-11-096-568A-29069	Sequence 29069, A
158	55	11.9	650	11	US-11-096-568A-29068	Sequence 29068, A
159	55	11.9	654	11	US-11-169-041-186	Sequence 186, App
160	55	11.9	726	11	US-11-188-298-3517	Sequence 3517, Ap
161	55	11.9	732	11	US-11-078-189-14	Sequence 14, Appl
162	55	11.9	756	11	US-11-188-298-5683	Sequence 5683, Ap
163	55	11.9	756	11	US-11-188-298-8848	Sequence 8848, Ap
164	55	11.9	786	9	US-10-485-310-10	Sequence 10, Appl
165	54.5	11.8	186	11	US-11-044-899-23	Sequence 23, Appl
166	54.5	11.8	189	11	US-11-096-568A-27999	Sequence 27999, A
167	54.5	11.8	189	11	US-11-096-568A-30670	Sequence 30670, A
168	54.5	11.8	197	11	US-11-096-568A-27998	Sequence 27998, A
169	54.5	11.8	197	11	US-11-096-568A-30669	Sequence 30669, A
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172	54.5	11.8	294	11	US-11-096-568A-32262	Sequence 32262, A
173	54.5	11.8	296	11	US-11-096-568A-32261	Sequence 32261, A
174	54.5	11.8	308	11	US-11-241-677-14	Sequence 14, Appl
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178	54.5	11.8	369	11	US-11-096-568A-28455	Sequence 28455, A
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181	54.5	11.8	373	11	US-11-096-568A-28453	Sequence 28453, A
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185	54.5	11.8	384	11	US-11-108-185-4	Sequence 4, Appli
186	54.5	11.8	384	11	US-11-087-099-9360	Sequence 9360, Ap
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189	54.5	11.8	422	11	US-11-087-099-1523	Sequence 1523, Ap
190	54.5	11.8	422	11	US-11-087-099-1957	Sequence 1957, Ap
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193	54.5	11.8	622	11	US-11-045-004-780	Sequence 780, App
194	54.5	11.8	809	11	US-11-188-298-13996	Sequence 13996, A
195	54.5	11.8	895	11	US-11-150-406-2	Sequence 2, Appli
196	54.5	11.8	920	9	US-10-821-234-1129	Sequence 1129, Ap
197	54	11.7	55	11	US-11-240-769-80	Sequence 80, Appl
198	54	11.7	139	11	US-11-096-568A-14847	Sequence 14847, A
199	54	11.7	143	11	US-11-087-099-767	Sequence 767, App
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201	54	11.7	194	11	US-11-096-568A-14846	Sequence 14846, A
202	54	11.7	237	11	US-11-096-568A-14845	Sequence 14845, A
203	54	11.7	246	11	US-11-096-568A-26953	Sequence 26953, A
204	54	11.7	249	11	US-11-096-568A-2861	Sequence 2861, Ap
205	54	11.7	253	11	US-11-096-568A-2860	Sequence 2860, Ap
206	54	11.7	253	11	US-11-096-568A-2862	Sequence 2862, Ap
207	54	11.7	277	11	US-11-096-568A-26952	Sequence 26952, A
208	54	11.7	316	11	US-11-188-298-2012	Sequence 2012, Ap
209	54	11.7	316	11	US-11-188-298-16808	Sequence 16808, A
210	54	11.7	316	11	US-11-188-298-19680	Sequence 19680, A
211	54	11.7	346	10	US-11-301-554-329	Sequence 329, App
212	54	11.7	346	11	US-11-186-284-189	Sequence 189, App
213	54	11.7	346	11	US-11-054-281-24	Sequence 24, Appl
214	54	11.7	346	11	US-11-054-281-96	Sequence 96, Appl
215	54	11.7	346	11	US-11-054-281-97	Sequence 97, Appl
216	54	11.7	348	11	US-11-054-281-69	Sequence 69, Appl
217	54	11.7	348	11	US-11-054-281-98	Sequence 98, Appl
218	54	11.7	348	11	US-11-054-281-99	Sequence 99, Appl
219	54	11.7	376	9	US-10-467-657-6138	Sequence 6138, Ap
220	54	11.7	404	11	US-11-188-298-5125	Sequence 5125, Ap
221	54	11.7	456	11	US-11-087-099-5433	Sequence 5433, Ap
222	54	11.7	456	11	US-11-087-099-6176	Sequence 6176, Ap
223	54	11.7	456	11	US-11-188-298-16004	Sequence 16004, A
224	54	11.7	558	11	US-11-045-004-782	Sequence 782, App
225	54	11.7	573	11	US-11-087-099-7597	Sequence 7597, Ap
226	54	11.7	573	11	US-11-188-298-6963	Sequence 6963, Ap
227	54	11.7	577	11	US-11-188-298-15674	Sequence 15674, A
228	54	11.7	711	11	US-11-188-298-9719	Sequence 9719, Ap
229	54	11.7	736	11	US-11-078-189-11	Sequence 11, Appl
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231	53.5	11.6	244	11	US-11-186-284-97	Sequence 97, Appl
232	53.5	11.6	244	11	US-11-050-857-670	Sequence 670, App
233	53.5	11.6	244	11	US-11-251-455-13	Sequence 13, Appl
234	53.5	11.6	253	11	US-11-050-857-671	Sequence 671, App
235	53.5	11.6	327	11	US-11-098-686-11321	Sequence 11321, A
236	53.5	11.6	407	9	US-10-793-626-1578	Sequence 1578, Ap
238	53.5	11.6	429	9	US-10-973-115B-94	Sequence 94, Appl
241	53.5	11.6	429	11	US-11-290-153-94	Sequence 94, Appl
242	53.5	11.6	482	11	US-11-096-568A-30946	Sequence 30946, A
243	53.5	11.6	485	11	US-11-096-568A-30945	Sequence 30945, A
244	53.5	11.6	495	9	US-10-613-744-5	Sequence 5, Appli
245	53.5	11.6	504	11	US-11-096-568A-30944	Sequence 30944, A
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247	53.5	11.6	593	11	US-11-188-298-14439	Sequence 14439, A
248	53.5	11.6	594	11	US-11-087-099-9040	Sequence 9040, Ap
249	53.5	11.6	594	11	US-11-188-298-8366	Sequence 8366, Ap
250	53.5	11.6	898	11	US-11-145-631-11	Sequence 11, Appl
251	53	11.5	165	11	US-11-072-512-2538	Sequence 2538, Ap
252	53	11.5	170	11	US-11-087-099-4479	Sequence 4479, Ap
253	53	11.5	223	11	US-11-055-822-1130	Sequence 1130, Ap
254	53	11.5	239	11	US-11-136-341A-2	Sequence 2, Appli
255	53	11.5	267	9	US-10-995-561-552	Sequence 552, App
256	53	11.5	267	9	US-10-995-561-553	Sequence 553, App
257	53	11.5	301	11	US-11-079-463-6653	Sequence 6653, Ap
258	53	11.5	309	11	US-11-087-099-3288	Sequence 3288, Ap
259	53	11.5	309	11	US-11-087-099-10759	Sequence 10759, A
260	53	11.5	376	11	US-11-188-298-1836	Sequence 1836, Ap
261	53	11.5	379	11	US-11-087-099-4820	Sequence 4820, Ap
262	53	11.5	394	11	US-11-188-298-17317	Sequence 17317, A
263	53	11.5	421	11	US-11-188-298-4276	Sequence 4276, Ap
264	53	11.5	469	11	US-11-188-298-2764	Sequence 2764, Ap
265	53	11.5	469	11	US-11-188-298-3864	Sequence 3864, Ap
266	53	11.5	469	11	US-11-188-298-4424	Sequence 4424, Ap
267	53	11.5	469	11	US-11-188-298-17299	Sequence 17299, A
268	53	11.5	469	11	US-11-188-298-17884	Sequence 17884, A
269	53	11.5	603	11	US-11-096-568A-28303	Sequence 28303, A
270	53	11.5	612	11	US-11-120-308-174	Sequence 174, App
271	53	11.5	701	11	US-11-096-568A-28302	Sequence 28302, A
272	53	11.5	776	11	US-11-096-568A-28301	Sequence 28301, A
273	53	11.5	776	11	US-11-188-298-446	Sequence 446, App
274	52.5	11.4	250	11	US-11-079-463-9349	Sequence 9349, Ap
275	52.5	11.4	292	11	US-11-096-568A-15102	Sequence 15102, A
276	52.5	11.4	292	11	US-11-096-568A-23663	Sequence 23663, A
277	52.5	11.4	321	11	US-11-096-568A-15101	Sequence 15101, A
278	52.5	11.4	321	11	US-11-096-568A-23662	Sequence 23662, A
279	52.5	11.4	354	11	US-11-096-568A-15100	Sequence 15100, A
280	52.5	11.4	354	11	US-11-096-568A-23661	Sequence 23661, A
281	52.5	11.4	357	11	US-11-096-568A-33734	Sequence 33734, A
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283	52.5	11.4	377	11	US-11-188-298-17198	Sequence 17198, A
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285	52.5	11.4	384	11	US-11-108-185-8	Sequence 8, Appli
286	52.5	11.4	384	11	US-11-108-185-10	Sequence 10, Appl

287	52.5	11.4	384	11	US-11-108-185-12	Sequence 12, Appl
288	52.5	11.4	463	11	US-11-124-367A-374	Sequence 374, App
289	52.5	11.4	468	11	US-11-087-099-4740	Sequence 4740, Ap
290	52.5	11.4	468	11	US-11-188-298-15353	Sequence 15353, A
291	52.5	11.4	496	11	US-11-087-099-4813	Sequence 4813, Ap
292	52.5	11.4	496	11	US-11-188-298-4413	Sequence 4413, Ap
293	52.5	11.4	612	11	US-11-172-740-1347	Sequence 1347, Ap
294	52.5	11.4	763	11	US-11-072-512-2766	Sequence 2766, Ap
295	52	11.3	95	11	US-11-152-366-277	Sequence 277, App
296	52	11.3	112	11	US-11-000-463-282	Sequence 282, App
297	52	11.3	112	11	US-11-000-463-754	Sequence 754, App
298	52	11.3	151	9	US-10-920-580-3	Sequence 3, Appli
299	52	11.3	151	9	US-10-920-876-3	Sequence 3, Appli
300	52	11.3	243	9	US-10-511-538-95	Sequence 95, Appl
301	52	11.3	243	9	US-10-537-002-66	Sequence 66, Appl
302	52	11.3	260	11	US-11-251-455-10	Sequence 10, Appl
303	52	11.3	310	11	US-11-010-795-22	Sequence 22, Appl
304	52	11.3	359	8	US-10-511-937-2932	Sequence 2932, Ap
305	52	11.3	359	8	US-10-511-937-2955	Sequence 2955, Ap
306	52	11.3	359	11	US-11-152-366-38	Sequence 38, Appl
307	52	11.3	378	11	US-11-082-389-404	Sequence 404, App
308	52	11.3	401	11	US-11-000-365-50	Sequence 50, Appl
309	52	11.3	401	11	US-11-032-794-50	Sequence 50, Appl
310	52	11.3	443	11	US-11-079-463-7888	Sequence 7888, Ap
311	52	11.3	444	11	US-11-087-099-1654	Sequence 1654, Ap
312	52	11.3	448	11	US-11-188-298-14870	Sequence 14870, A
313	52	11.3	450	11	US-11-188-298-19216	Sequence 19216, A
314	52	11.3	462	11	US-11-087-099-744	Sequence 744, App
315	52	11.3	467	11	US-11-087-099-10123	Sequence 10123, A
316	52	11.3	467	11	US-11-188-298-20347	Sequence 20347, A
317	52	11.3	485	11	US-11-188-298-6318	Sequence 6318, Ap
318	52	11.3	624	11	US-11-188-298-13475	Sequence 13475, A
319	52	11.3	628	11	US-11-082-389-402	Sequence 402, App
320	52	11.3	628	11	US-11-188-298-4635	Sequence 4635, Ap
321	52	11.3	630	11	US-11-188-298-8854	Sequence 8854, Ap
322	52	11.3	711	9	US-10-467-657-2966	Sequence 2966, Ap
323	52	11.3	772	11	US-11-188-298-4025	Sequence 4025, Ap
324	52	11.3	773	11	US-11-188-298-15538	Sequence 15538, A
325	52	11.3	829	11	US-11-188-298-17291	Sequence 17291, A
340	52	11.3	2138	9	US-10-784-004-639	Sequence 639, App
341	52	11.3	2221	11	US-11-126-313-30	Sequence 30, Appl
342	51.5	11.2	59	9	US-10-689-742-174	Sequence 174, App
343	51.5	11.2	112	11	US-11-176-830-614	Sequence 614, App
344	51.5	11.2	123	11	US-11-072-512-2234	Sequence 2234, Ap
351	51.5	11.2	211	9	US-10-965-972-1	Sequence 1, Appli
357	51.5	11.2	211	11	US-11-186-284-22	Sequence 22, Appl
358	51.5	11.2	212	8	US-10-505-928-298	Sequence 298, App
359	51.5	11.2	212	11	US-11-288-493-68	Sequence 68, Appl
360	51.5	11.2	244	9	US-10-510-386-110	Sequence 110, App
361	51.5	11.2	245	11	US-11-096-568A-10277	Sequence 10277, A
363	51.5	11.2	307	9	US-10-203-486-4	Sequence 4, Appli
368	51.5	11.2	309	11	US-11-188-298-8107	Sequence 8107, Ap
369	51.5	11.2	312	11	US-11-082-389-346	Sequence 346, App
370	51.5	11.2	327	11	US-11-096-568A-4231	Sequence 4231, Ap
371	51.5	11.2	349	11	US-11-096-568A-4230	Sequence 4230, Ap
372	51.5	11.2	370	11	US-11-045-004-127	Sequence 127, App
373	51.5	11.2	373	11	US-11-096-568A-4229	Sequence 4229, Ap
374	51.5	11.2	378	11	US-11-096-568A-4595	Sequence 4595, Ap
375	51.5	11.2	380	11	US-11-087-099-6739	Sequence 6739, Ap
376	51.5	11.2	382	11	US-11-124-368A-173	Sequence 173, App
377	51.5	11.2	382	11	US-11-124-368A-174	Sequence 174, App
378	51.5	11.2	382	11	US-11-127-877-58	Sequence 58, Appl
379	51.5	11.2	388	11	US-11-096-568A-4594	Sequence 4594, Ap
380	51.5	11.2	392	11	US-11-087-099-9117	Sequence 9117, Ap
381	51.5	11.2	409	11	US-11-096-568A-4593	Sequence 4593, Ap
382	51.5	11.2	468	11	US-11-096-568A-22859	Sequence 22859, A
383	51.5	11.2	469	11	US-11-087-099-321	Sequence 321, App
384	51.5	11.2	469	11	US-11-087-099-6164	Sequence 6164, Ap
385	51.5	11.2	469	11	US-11-188-298-12633	Sequence 12633, A
386	51.5	11.2	510	11	US-11-096-568A-22858	Sequence 22858, A
387	51.5	11.2	537	11	US-11-179-958A-2	Sequence 2, Appli
388	51.5	11.2	543	11	US-11-087-099-4195	Sequence 4195, Ap
389	51.5	11.2	766	11	US-11-188-298-9041	Sequence 9041, Ap
390	51.5	11.2	808	11	US-11-072-512-2654	Sequence 2654, Ap
391	51.5	11.2	1003	11	US-11-188-298-8292	Sequence 8292, Ap
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393	51.5	11.2	1167	9	US-10-455-772-990	Sequence 990, App
394	51.5	11.2	1167	9	US-10-455-772-992	Sequence 992, App
395	51.5	11.2	1204	9	US-10-455-772-988	Sequence 988, App
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398	51	11.1	155	11	US-11-188-298-18515	Sequence 18515, A
399	51	11.1	195	11	US-11-188-298-4538	Sequence 4538, Ap
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404	51	11.1	261	11	US-11-096-568A-4271	Sequence 4271, Ap
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410	51	11.1	327	11	US-11-096-568A-4269	Sequence 4269, Ap
411	51	11.1	329	11	US-11-096-568A-3311	Sequence 3311, Ap
412	51	11.1	354	11	US-11-096-568A-3310	Sequence 3310, Ap
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431	51	11.1	774	11	US-11-000-463-459	Sequence 459, App
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438	51	11.1	967	11	US-11-054-281-75	Sequence 75, Appl
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448	50.5	11.0	207	9	US-10-931-198-66	Sequence 66, Appl
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524	50	10.8	346	11	US-11-032-794-52	Sequence 52, Appl
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526	50	10.8	351	11	US-11-054-281-100	Sequence 100, App
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536	50	10.8	457	9	US-10-982-545-13	Sequence 13, Appl
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552	49.5	10.7	204	11	US-11-033-039-271	Sequence 271, App
553	49.5	10.7	218	11	US-11-045-004-648	Sequence 648, App
554	49.5	10.7	236	11	US-11-096-568A-4557	Sequence 4557, Ap
555	49.5	10.7	252	9	US-10-821-234-1445	Sequence 1445, Ap
556	49.5	10.7	252	9	US-10-986-405-198	Sequence 198, App
557	49.5	10.7	252	11	US-11-186-284-8	Sequence 8, Appli
558	49.5	10.7	252	11	US-11-172-610-11	Sequence 11, Appl
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562	49.5	10.7	285	11	US-11-079-463-6287	Sequence 6287, Ap
563	49.5	10.7	296	11	US-11-229-769-293	Sequence 293, App
564	49.5	10.7	303	11	US-11-188-298-18841	Sequence 18841, A
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571	49.5	10.7	380	11	US-11-087-099-4713	Sequence 4713, Ap
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574	49.5	10.7	414	9	US-10-793-626-806	Sequence 806, App
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583	49.5	10.7	557	11	US-11-191-375-4	Sequence 4, Appli
584	49.5	10.7	557	11	US-11-191-588-4	Sequence 4, Appli
585	49.5	10.7	576	11	US-11-087-099-10787	Sequence 10787, A
586	49.5	10.7	576	11	US-11-172-740-973	Sequence 973, App
587	49.5	10.7	628	11	US-11-183-136-12	Sequence 12, Appl
588	49.5	10.7	640	11	US-11-188-298-11801	Sequence 11801, A
589	49.5	10.7	656	11	US-11-079-463-7923	Sequence 7923, Ap
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594	49.5	10.7	660	11	US-11-290-153-350	Sequence 350, App
595	49.5	10.7	694	11	US-11-098-686-10456	Sequence 10456, A
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597	49.5	10.7	785	11	US-11-087-099-9941	Sequence 9941, Ap
598	49.5	10.7	960	11	US-11-087-099-8676	Sequence 8676, Ap
599	49.5	10.7	1461	11	US-11-052-554A-283	Sequence 283, App
600	49	10.6	92	11	US-11-174-413-67	Sequence 67, Appl
601	49	10.6	167	11	US-11-103-957-63	Sequence 63, Appl
602	49	10.6	198	11	US-11-079-463-8373	Sequence 8373, Ap
603	49	10.6	203	11	US-11-096-568A-1465	Sequence 1465, Ap
604	49	10.6	225	11	US-11-087-099-4799	Sequence 4799, Ap
605	49	10.6	239	11	US-11-136-341A-3	Sequence 3, Appli
606	49	10.6	254	11	US-11-096-568A-31683	Sequence 31683, A
607	49	10.6	254	11	US-11-188-298-17103	Sequence 17103, A
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609	49	10.6	276	9	US-10-467-657-4158	Sequence 4158, Ap
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611	49	10.6	318	11	US-11-146-428-54	Sequence 54, Appl
612	49	10.6	320	11	US-11-188-298-20415	Sequence 20415, A
613	49	10.6	325	11	US-11-188-298-12687	Sequence 12687, A
614	49	10.6	332	11	US-11-188-298-20879	Sequence 20879, A
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620	49	10.6	352	11	US-11-068-686-2	Sequence 2, Appli
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623	49	10.6	361	11	US-11-188-298-19581	Sequence 19581, A
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635	49	10.6	440	11	US-11-096-568A-31681	Sequence 31681, A
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637	49	10.6	458	11	US-11-087-099-9665	Sequence 9665, Ap
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639	49	10.6	458	11	US-11-045-004-1603	Sequence 1603, Ap
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661	49	10.6	740	11	US-11-124-367A-293	Sequence 293, App
662	49	10.6	760	11	US-11-124-367A-292	Sequence 292, App
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666	49	10.6	826	11	US-11-087-099-6618	Sequence 6618, Ap
667	49	10.6	908	11	US-11-199-233-15	Sequence 15, Appl
668	49	10.6	914	9	US-10-537-002-60	Sequence 60, Appl
669	49	10.6	914	11	US-11-108-172-1066	Sequence 1066, Ap
670	49	10.6	914	11	US-11-148-108-41	Sequence 41, Appl
671	49	10.6	914	11	US-11-264-096-2054	Sequence 2054, Ap
672	49	10.6	991	11	US-11-096-568A-30055	Sequence 30055, A
673	49	10.6	994	11	US-11-096-568A-30054	Sequence 30054, A
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678	49	10.6	1023	11	US-11-290-153-200	Sequence 200, App
679	49	10.6	1070	9	US-10-537-002-14	Sequence 14, Appl
680	49	10.6	1073	9	US-10-537-002-11	Sequence 11, Appl
681	49	10.6	1197	11	US-11-087-099-8238	Sequence 8238, Ap
682	49	10.6	3343	11	US-11-122-396-7	Sequence 7, Appli
683	48.5	10.5	57	9	US-10-207-797-162	Sequence 162, App
684	48.5	10.5	112	11	US-11-176-830-209	Sequence 209, App
685	48.5	10.5	112	11	US-11-176-830-603	Sequence 603, App
686	48.5	10.5	112	11	US-11-176-830-604	Sequence 604, App
687	48.5	10.5	112	11	US-11-176-830-607	Sequence 607, App
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693	48.5	10.5	112	11	US-11-176-830-618	Sequence 618, App
694	48.5	10.5	112	11	US-11-176-830-619	Sequence 619, App
695	48.5	10.5	112	11	US-11-176-830-620	Sequence 620, App
696	48.5	10.5	112	11	US-11-176-830-621	Sequence 621, App
697	48.5	10.5	112	11	US-11-176-830-622	Sequence 622, App
698	48.5	10.5	112	11	US-11-176-830-623	Sequence 623, App
699	48.5	10.5	112	11	US-11-176-830-624	Sequence 624, App
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701	48.5	10.5	112	11	US-11-176-830-626	Sequence 626, App
702	48.5	10.5	112	11	US-11-176-830-627	Sequence 627, App
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704	48.5	10.5	112	11	US-11-176-830-629	Sequence 629, App
705	48.5	10.5	112	11	US-11-176-830-630	Sequence 630, App
706	48.5	10.5	113	11	US-11-149-309-32	Sequence 32, Appl
707	48.5	10.5	113	11	US-11-155-843-124	Sequence 124, App
708	48.5	10.5	132	11	US-11-149-309-31	Sequence 31, Appl
709	48.5	10.5	132	11	US-11-155-843-178	Sequence 178, App
710	48.5	10.5	136	11	US-11-051-267-29	Sequence 29, Appl
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724	48.5	10.5	293	11	US-11-096-568A-19465	Sequence 19465, A
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739	48.5	10.5	404	11	US-11-072-512-3621	Sequence 3621, Ap
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741	48.5	10.5	442	10	US-11-264-784-9	Sequence 9, Appli
742	48.5	10.5	462	11	US-11-188-298-8905	Sequence 8905, Ap
743	48.5	10.5	485	11	US-11-087-099-9429	Sequence 9429, Ap
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757	48.5	10.5	608	11	US-11-087-099-3204	Sequence 3204, Ap
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761	48.5	10.5	616	9	US-10-501-035-384	Sequence 384, App
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763	48.5	10.5	638	11	US-11-188-298-14582	Sequence 14582, A
764	48.5	10.5	638	11	US-11-188-298-18598	Sequence 18598, A
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773	48.5	10.5	778	9	US-10-505-263-81	Sequence 81, Appl
774	48.5	10.5	789	9	US-10-506-454-597	Sequence 597, App
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777	48.5	10.5	1954	9	US-10-784-004-1235	Sequence 1235, Ap
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779	48	10.4	37	9	US-10-219-783-9	Sequence 9, Appli
780	48	10.4	68	9	US-10-467-657-4718	Sequence 4718, Ap
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782	48	10.4	74	11	US-11-229-769-229	Sequence 229, App
783	48	10.4	100	11	US-11-172-740-651	Sequence 651, App
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787	48	10.4	212	9	US-10-506-454-635	Sequence 635, App
788	48	10.4	215	11	US-11-096-568A-17652	Sequence 17652, A
789	48	10.4	220	11	US-11-045-004-2623	Sequence 2623, Ap
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802	48	10.4	285	11	US-11-188-298-7544	Sequence 7544, Ap
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833	48	10.4	531	11	US-11-188-298-21763	Sequence 21763, A
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836	48	10.4	573	11	US-11-188-298-8148	Sequence 8148, Ap
837	48	10.4	573	11	US-11-188-298-9722	Sequence 9722, Ap
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839	48	10.4	601	11	US-11-072-512-2034	Sequence 2034, Ap
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844	48	10.4	713	8	US-10-505-928-345	Sequence 345, App
845	48	10.4	729	11	US-11-087-099-5269	Sequence 5269, Ap
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847	48	10.4	840	9	US-10-725-475-16	Sequence 16, Appl
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849	48	10.4	869	11	US-11-043-752-45	Sequence 45, Appl
850	48	10.4	922	9	US-10-517-939-38	Sequence 38, Appl
851	48	10.4	929	11	US-11-087-099-6648	Sequence 6648, Ap
852	48	10.4	929	11	US-11-087-099-7898	Sequence 7898, Ap
853	48	10.4	948	9	US-10-485-517-131	Sequence 131, App
854	48	10.4	959	11	US-11-188-298-12621	Sequence 12621, A
855	48	10.4	1024	9	US-10-455-772-784	Sequence 784, App
856	48	10.4	1024	9	US-10-455-772-788	Sequence 788, App
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861	48	10.4	1478	11	US-11-188-298-8632	Sequence 8632, Ap
862	48	10.4	1478	11	US-11-188-298-13053	Sequence 13053, A
863	48	10.4	1908	9	US-10-915-002-314	Sequence 314, App
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865	47.5	10.3	89	11	US-11-123-896-245	Sequence 245, App
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867	47.5	10.3	107	11	US-11-123-896-269	Sequence 269, App
868	47.5	10.3	112	11	US-11-176-830-608	Sequence 608, App
869	47.5	10.3	122	7	US-09-995-493-42	Sequence 42, Appl
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871	47.5	10.3	184	11	US-11-153-071-10	Sequence 10, Appl
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874	47.5	10.3	212	11	US-11-096-568A-6211	Sequence 6211, Ap
875	47.5	10.3	215	9	US-10-506-454-623	Sequence 623, App
876	47.5	10.3	239	11	US-11-096-568A-33024	Sequence 33024, A
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878	47.5	10.3	243	11	US-11-096-568A-8143	Sequence 8143, Ap
879	47.5	10.3	245	11	US-11-096-568A-6210	Sequence 6210, Ap
880	47.5	10.3	247	9	US-10-506-454-1384	Sequence 1384, Ap
881	47.5	10.3	247	11	US-11-087-099-12410	Sequence 12410, A
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908	47.5	10.3	383	11	US-11-096-568A-8034	Sequence 8034, Ap
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913	47.5	10.3	396	11	US-11-087-099-8866	Sequence 8866, Ap
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925	47.5	10.3	491	9	US-10-506-454-1574	Sequence 1574, Ap
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927	47.5	10.3	498	11	US-11-188-298-5913	Sequence 5913, Ap
928	47.5	10.3	498	11	US-11-188-298-8627	Sequence 8627, Ap
929	47.5	10.3	508	11	US-11-096-568A-15743	Sequence 15743, A
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1462	46	10.0	756	9	US-10-055-877-189	Sequence 189, App
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1484	46	10.0	3028	9	US-10-455-772-286	Sequence 286, App
1485	46	10.0	3028	9	US-10-455-772-288	Sequence 288, App
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1487	45.5	9.9	47	11	US-11-264-096-479	Sequence 479, App
1488	45.5	9.9	119	9	US-10-467-657-4694	Sequence 4694, Ap
1489	45.5	9.9	121	11	US-11-070-992A-4	Sequence 4, Appli
1490	45.5	9.9	126	11	US-11-188-298-7168	Sequence 7168, Ap
1491	45.5	9.9	137	11	US-11-183-261-44	Sequence 44, Appl
1492	45.5	9.9	138	11	US-11-080-991-12	Sequence 12, Appl
1493	45.5	9.9	145	11	US-11-246-980-3	Sequence 3, Appli
1494	45.5	9.9	155	7	US-09-978-360A-456	Sequence 456, App
1495	45.5	9.9	158	11	US-11-079-463-7765	Sequence 7765, Ap
1496	45.5	9.9	163	11	US-11-188-298-13544	Sequence 13544, A
1497	45.5	9.9	171	11	US-11-188-298-11672	Sequence 11672, A
1498	45.5	9.9	175	9	US-10-467-657-7504	Sequence 7504, Ap
1499	45.5	9.9	176	11	US-11-188-298-8191	Sequence 8191, Ap
1500	45.5	9.9	179	7	US-09-995-493-134	Sequence 134, App

Search completed: May 12, 2006, 21:44:32
Job time : 29 secs

OM protein - protein search, using sw model

Run on: May 12, 2006, 21:19:29.; Search time 39 Seconds
(without alignments)
219.572 Million cell updates/sec

Title: US-10-063-557-50
Perfect score: 461
Sequence: 1 MERVTLALLLLAGLTALEAN.....HSPVPEKAIPLITPGSATTC 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	256.5	55.6	87	2	I59391	transmembrane prot
2	241.5	52.4	88	2	S61552	mammary tumor prot
3	214.5	46.5	87	2	A55571	chloride conductan
4	126.5	27.4	92	2	A40533	cAMP-dependent pro
5	96.5	20.9	58	2	D46435	Na+/K+-exchanging
6	94.5	20.5	53	2	A46435	Na+/K+-exchanging
7	75.5	16.4	58	2	B46435	Na+/K+-exchanging
8	73.5	15.9	58	2	C46435	Na+/K+-exchanging
9	72	15.6	160	1	A61088	plastoquinol-plast
10	71	15.4	529	2	F69989	conserved hypothet
11	69	15.0	150	2	AH0371	probable membrane
12	67.5	14.6	135	2	A05009	hypothetical prote
13	66.5	14.4	359	2	B86620	chorismate synthas
14	66.5	14.4	359	2	A72004	chorismate synthas
15	66.5	14.4	523	2	A38101	potassium channel
16	66	14.3	446	2	B90463	proline/betaine tr
17	64	13.9	525	2	A43531	potassium channel
18	63.5	13.8	309	2	AC1697	probable transport
19	63.5	13.8	309	2	AI1325	probable transport
20	63.5	13.8	511	2	A46020	potassium channel
21	63.5	13.8	511	2	S07095	potassium channel
22	63.5	13.8	585	2	A39395	delayed rectifier
23	63.5	13.8	620	2	A70525	hypothetical prote
24	63	13.7	468	2	C96818	hypothetical prote
25	62.5	13.6	299	2	A38111	transcription regu
26	62.5	13.6	679	2	A42073	potassium channel
27	62.5	13.6	769	2	I56546	Shaw type potassiu
28	62.5	13.6	910	2	F81974	leucine-tRNA ligas
29	62	13.4	381	2	AB2907	GGDEF family prote
30	62	13.4	393	2	B97682	ggdef family prote
31	62	13.4	589	2	T43295	uracil transport p
32	62	13.4	777	2	S30271	pyocin AP41 large
33	61.5	13.3	342	2	S75086	iron-stress chloro
34	61.5	13.3	433	2	B72025	flagellum-specific
35	61.5	13.3	433	2	A81513	virulence ATPase,
36	61.5	13.3	433	2	H86597	flagellum-specific
37	61.5	13.3	445	2	AD0962	DsdX permease [imp
38	61.5	13.3	990	2	JC8058	laeverin - human
39	61.5	13.3	1499	2	AC2555	hypothetical prote
40	61	13.2	268	2	C87295	conserved hypothet
41	61	13.2	355	2	I51157	major histocompati
42	61	13.2	461	2	B90984	O antigen flippase
43	61	13.2	463	2	A75151	damage-inducible p
44	61	13.2	463	2	E85829	O antigen flippase
45	61	13.2	463	2	G71191	probable DNA damag
46	61	13.2	520	2	D84471	probable membrane
47	60.5	13.1	295	2	C84830	probable protein k
48	60.5	13.1	312	2	B83749	sugar transport sy
49	60.5	13.1	326	2	C90272	hypothetical prote
50	60.5	13.1	354	2	G86276	hypothetical prote
51	60.5	13.1	427	2	E87669	conserved hypothet
52	60.5	13.1	463	2	AI0388	probable proline-s
53	60.5	13.1	516	2	T47509	probable transport
54	60.5	13.1	581	2	S17150	potassium channel
55	60.5	13.1	613	2	A39402	potassium channel
56	60.5	13.1	624	2	S22703	voltage-gated pota
57	60.5	13.1	728	2	B81370	phosphoribosylform
58	60	13.0	71	2	C23876	vitellogenin B1 pr
59	60	13.0	208	2	S36155	paired box protein
60	60	13.0	269	2	AH1970	type 4 prepilin pe
61	60	13.0	342	2	S57652	transcription fact
62	60	13.0	412	2	A83461	hypothetical prote
63	60	13.0	497	1	WMBELM	membrane protein L
64	60	13.0	538	2	A65175	hypothetical 60.6
65	60	13.0	5232	2	A45086	HC-toxin synthetas
66	59.5	12.9	267	2	G86782	phosphomethylpyrim
67	59.5	12.9	298	2	A82387	amino acid ABC tra
68	59.5	12.9	356	2	T30361	occlusion-derived
69	59.5	12.9	527	2	A48076	glucose transporte
70	59.5	12.9	527	2	A45611	probable hexose tr
71	59	12.8	130	2	B85808	unknown protein en
72	59	12.8	175	2	T11087	NADH2 dehydrogenas
73	59	12.8	177	2	AH1669	probable NAD(P)H o
74	59	12.8	215	2	E85704	probable channel p
75	59	12.8	215	2	F90846	probable channel p
76	59	12.8	215	2	E64871	probable membrane
77	59	12.8	310	2	G87624	integral membrane
78	59	12.8	326	2	AB3607	3-oxoacyl-[acyl-ca
79	59	12.8	419	2	E90446	permease [imported
80	59	12.8	420	2	G96002	probable sugar upt
81	59	12.8	479	2	C95366	NADH2 dehydrogenas
82	59	12.8	558	2	AB1599	glycerol 3 phospha
83	59	12.8	653	2	A39922	potassium channel
84	59	12.8	654	2	S11049	potassium channel
85	59	12.8	660	2	S24125	potassium channel
86	59	12.8	802	2	JH0595	potassium channel
87	59	12.8	853	1	CHRTD1	potassium channel
88	59	12.8	857	2	I56529	potassium channel
89	59	12.8	858	2	S31761	potassium channel
90	58.5	12.7	182	2	C83600	hypothetical prote
91	58.5	12.7	384	2	AI2962	cellulose synthesi
92	58.5	12.7	389	2	E98320	hypothetical prote
93	58.5	12.7	411	2	H75376	hypothetical prote
94	58.5	12.7	425	2	T50355	hypothetical prote
95	58.5	12.7	463	2	D87201	conserved hypothet
96	58.5	12.7	633	2	E86271	protein F16A14.4 [
97	58.5	12.7	876	2	G81029	leucine-tRNA ligas
98	58.5	12.7	1095	2	E96744	probable oligopept
99	58.5	12.7	1189	2	I39711	celE protein - Agr
100	58.5	12.7	2712	2	T30949	hypothetical prote
101	58.5	12.7	3864	2	D87757	protein C44E4.1a [
102	58	12.6	114	2	F69782	hypothetical prote

103	58	12.6	185	2	AG1054	probable exported
104	58	12.6	196	2	E75612	hypothetical prote
105	58	12.6	215	2	AF0650	probable membrane
106	58	12.6	257	2	A64459	diphthine synthase
107	58	12.6	277	2	S44252	raffinose operon r
108	58	12.6	368	2	T26425	hypothetical prote
109	58	12.6	376	2	AH1795	hypothetical membr
110	58	12.6	398	2	A82081	cell division prot
111	58	12.6	462	2	F75588	probable kynurenin
112	58	12.6	4836	2	T14346	herc2 protein - mo
113	57.5	12.5	71	2	D23876	vitellogenin B2 pr
114	57.5	12.5	139	2	AF0685	hypothetical prote
115	57.5	12.5	324	2	T36805	conserved hypothet
116	57.5	12.5	342	2	A47673	photosystem II chl
117	57.5	12.5	356	2	C72475	hypothetical prote
118	57.5	12.5	374	2	T10415	virus envelope pro
119	57.5	12.5	461	2	B83601	probable transport
120	57.5	12.5	461	2	AF0579	C4-dicarboxylate a
121	57.5	12.5	523	2	B83629	probable ATP-bindi
122	57.5	12.5	528	2	I84205	potassium channel
123	57.5	12.5	594	2	B90586	transport protein
124	57.5	12.5	636	2	S47299	gene F protein - r
125	57.5	12.5	662	2	T44219	hypothetical prote
126	57.5	12.5	662	2	T44034	hypothetical prote
127	57.5	12.5	1902	1	B44858	lactocepin (EC 3.4
128	57	12.4	148	2	C84690	probable membrane
129	57	12.4	185	2	JN0766	adrenomedullin pre
130	57	12.4	258	2	F71251	probable uridine p
131	57	12.4	269	2	AG2268	hypothetical prote
132	57	12.4	342	2	A30189	iron stress-induce
133	57	12.4	374	2	T05660	hypothetical prote
134	57	12.4	374	2	T00561	nodulin-like prote
135	57	12.4	385	2	T04725	hypothetical prote
136	57	12.4	440	2	H86312	F2H15.2 protein -
137	57	12.4	456	2	H96902	membrane protein,
138	57	12.4	457	2	B64769	proline transport
139	57	12.4	457	2	D90685	proline permease t
140	57	12.4	457	2	H85535	proline permease t
141	57	12.4	461	2	D90711	c4-dicarboxylate a
142	57	12.4	461	2	C64796	dcuC protein - Esc
143	57	12.4	461	2	H85561	transport of dicar
144	57	12.4	487	2	S73277	photosystem II 44K
145	56.5	12.3	114	2	E43559	homeotic protein R
146	56.5	12.3	187	2	S70186	21K protein - Shig
147	56.5	12.3	191	2	AD0905	probable exported
148	56.5	12.3	233	2	F70668	probable lipoprote
149	56.5	12.3	258	2	D84336	uridine phosphoryl
150	56.5	12.3	361	2	S19552	potassium channel
151	56.5	12.3	419	2	S22136	endothiapepsin (EC
152	56.5	12.3	471	2	T04911	hypothetical prote
153	56.5	12.3	485	2	E97506	potassium uptake p
154	56.5	12.3	500	2	F97025	spoVB related memb
155	56.5	12.3	614	2	A69845	Na+/H+ antiporter
156	56.5	12.3	670	1	E70040	conserved hypothet
157	56.5	12.3	686	1	VGBENA	glycoprotein H pre
158	56.5	12.3	686	1	VGBEPK	glycoprotein H pre
159	56.5	12.3	686	2	S15478	glycoprotein H - s
160	56.5	12.3	852	2	S25359	hypothetical prote
161	56	12.1	79	1	TIEPVK	K+ channel blocker
162	56	12.1	196	2	F64231	hypothetical prote
163	56	12.1	222	2	F82353	conserved hypothet
164	56	12.1	261	2	AB2966	conserved hypothet
165	56	12.1	261	2	B98317	ATP synthase chain
166	56	12.1	388	2	T09885	hypothetical prote
167	56	12.1	411	2	C87586	metal ion efflux m
168	56	12.1	436	2	G70058	hypothetical prote
169	56	12.1	440	2	C97376	probable transport
170	56	12.1	440	2	AI2593	MFS permease [impo
171	56	12.1	449	2	H70546	hypothetical prote
172	56	12.1	503	2	S36514	L1 protein - human
173	56	12.1	547	2	D95337	probable manganese
174	56	12.1	558	2	S29125	dimethylaniline mo
175	56	12.1	578	2	B37852	phosphotransferase
176	56	12.1	594	2	A83096	probable permease
177	56	12.1	626	2	D70178	PTS system, fructo
178	56	12.1	736	2	C69451	cationic amino aci
179	56	12.1	1118	2	C95385	probable adenylate
180	56	12.1	1305	2	AB0168	probable cell divi
181	56	12.1	2055	2	T30259	multiple PDZ domai
182	56	12.1	3329	2	T42205	breast cancer susc
183	56	12.1	5170	2	T15348	hypothetical prote
184	55.5	12.0	245	2	A90527	hypothetical prote
185	55.5	12.0	249	4	T44821	bacteriorhodopsin
186	55.5	12.0	254	2	F75496	conserved hypothet
187	55.5	12.0	256	2	E75401	hypothetical prote
188	55.5	12.0	259	4	T44820	bacteriorhodopsin
189	55.5	12.0	262	1	RAHSB	bacteriorhodopsin
190	55.5	12.0	262	2	H84300	bacteriorhodopsin
191	55.5	12.0	270	2	B29934	pancreatic elastas
192	55.5	12.0	299	2	B83243	hypothetical prote
193	55.5	12.0	309	2	C95138	tagatose-6-phospha
194	55.5	12.0	309	2	A98006	tagatose-6-phospha
195	55.5	12.0	316	2	G75388	hypothetical prote
196	55.5	12.0	317	2	S16299	exoZ protein - Rhi
197	55.5	12.0	317	2	B95975	acetyltransferase
198	55.5	12.0	344	2	S42648	photosystem II chl
199	55.5	12.0	344	2	AB2306	photosystem II chl
200	55.5	12.0	346	2	C71042	probable threonine
201	55.5	12.0	376	2	F72868	occlusion-derived
202	55.5	12.0	383	2	S53379	probable membrane
203	55.5	12.0	385	2	F86464	hypothetical prote
204	55.5	12.0	389	2	B81347	probable aspartate
205	55.5	12.0	456	2	T22347	hypothetical prote
206	55.5	12.0	459	2	D86669	amino acid permeas
207	55.5	12.0	545	2	AI2327	hypothetical prote
208	55.5	12.0	609	2	S28283	hypothetical prote
209	55.5	12.0	625	2	S13919	potassium channel
210	55.5	12.0	648	2	C71658	probable primosoma
211	55.5	12.0	716	2	T03695	delta 1 pyrroline-
212	55.5	12.0	851	2	T12503	hypothetical prote
213	55.5	12.0	946	1	A29550	methylenetetrahydr
214	55.5	12.0	1217	2	T22672	hypothetical prote
215	55.5	12.0	1423	2	A49206	exo-beta-D-fructos
216	55.5	12.0	2054	2	T46612	multi PDZ domain p
217	55	11.9	52	2	T32956	hypothetical prote
218	55	11.9	52	2	T33694	hypothetical prote
219	55	11.9	128	2	F71371	hypothetical prote
220	55	11.9	169	2	S18653	hypothetical prote
221	55	11.9	212	2	E82125	conserved hypothet
222	55	11.9	268	2	S05471	embryonic abundant
223	55	11.9	268	2	S14068	seed protein precu
224	55	11.9	288	2	T12462	hypothetical prote
225	55	11.9	312	2	B75405	endopeptidase-rela
226	55	11.9	334	2	S54438	hemin permease [va
227	55	11.9	336	2	AH0201	probable Zinc-bind
228	55	11.9	340	2	AF2896	hypothetical prote
229	55	11.9	340	2	H97671	hypothetical prote
230	55	11.9	344	2	E84043	glyceraldehyde-3-p
231	55	11.9	357	2	A23641	RP2 protein, testo
232	55	11.9	376	1	S17246	chorismate synthas
233	55	11.9	404	2	S34031	KTR3 protein - yea
234	55	11.9	410	2	AH2895	hypothetical prote
235	55	11.9	410	2	C97671	probable maltose-b
236	55	11.9	443	2	B86180	protein T1G11.3 [i
237	55	11.9	459	2	A87201	conserved hypothet
238	55	11.9	461	2	S57713	probable mannosyl
239	55	11.9	473	1	F2KK4C	photosystem II chl
240	55	11.9	482	2	AG1147	P60 extracellular
241	55	11.9	484	2	A41487	protein P60 precur
242	55	11.9	654	2	A96235	hydroxamate-depend
243	55	11.9	654	2	AC3051	hypothetical prote
244	55	11.9	716	2	E69672	penicillin-binding
245	55	11.9	2531	2	S18188	notch protein homo
246	55	11.9	2531	2	A46019	notch-1 protein -
247	54.5	11.8	173	2	S33295	translocon-associa
248	54.5	11.8	177	2	G75285	hypothetical prote

249	54.5	11.8	185	2	T51844	RING-H2 finger pro
250	54.5	11.8	204	2	AC1961	ATP-dependent Clp
251	54.5	11.8	226	2	S76020	endopeptidase Clp
252	54.5	11.8	255	2	F86203	hypothetical prote
253	54.5	11.8	269	2	T19947	hypothetical prote
254	54.5	11.8	276	2	AC1838	hypothetical prote
255	54.5	11.8	282	2	PQ0376	cell fusion glycop
256	54.5	11.8	296	2	F83145	probable epoxide h
257	54.5	11.8	296	2	A85698	transposase for IS
258	54.5	11.8	296	2	A99840	transposase for IS
259	54.5	11.8	304	2	S59965	phosphotransferase
260	54.5	11.8	337	2	G87487	conserved hypothet
261	54.5	11.8	362	2	S77244	biotin synthase (E
262	54.5	11.8	369	2	E81722	hypothetical prote
263	54.5	11.8	373	2	G85355	nodulin-like prote
264	54.5	11.8	393	2	AB0035	cystathionine beta
265	54.5	11.8	422	2	T07967	mandelonitrile lya
266	54.5	11.8	445	1	S54140	D-serine permease
267	54.5	11.8	458	1	YTBSRT	tetracycline resis
268	54.5	11.8	458	1	YTSOG	tetracycline resis
269	54.5	11.8	458	1	YTBSU6	tetracycline resis
270	54.5	11.8	458	2	JQ1211	tetracycline resis
271	54.5	11.8	458	2	S23743	tetracycline resis
272	54.5	11.8	483	1	A53595	allantoinase (EC 3
273	54.5	11.8	484	2	T00158	amidase (EC 3.5.-.
274	54.5	11.8	501	2	E87239	aldehyde dehydroge
275	54.5	11.8	576	2	A49933	proteinase SM tran
276	54.5	11.8	586	2	T48672	ABC-type transport
277	54.5	11.8	622	2	AC1236	acyltransferase (t
278	54.5	11.8	628	2	T01467	hypothetical prote
279	54.5	11.8	722	2	B71728	probable peptidase
280	54.5	11.8	735	2	E69139	hypothetical prote
281	54.5	11.8	895	2	I54343	dystroglycan - hum
282	54.5	11.8	895	2	S20582	dystrophin-associa
283	54.5	11.8	900	2	G87431	pyruvate phosphate
284	54.5	11.8	1044	2	T31072	heterocyst differe
285	54.5	11.8	1044	2	AB2158	heterocyst differe
286	54.5	11.8	1099	2	T14850	S-layer protein pr
287	54.5	11.8	1146	2	B35962	protein-tyrosine k
288	54.5	11.8	1182	2	A35962	protein-tyrosine k
289	54	11.7	98	2	T17183	NADH2 dehydrogenas
290	54	11.7	98	2	T17348	NADH2 dehydrogenas
291	54	11.7	154	1	MMBEI6	16.9K membrane pro
292	54	11.7	168	2	S47881	NADH2 dehydrogenas
293	54	11.7	188	2	A75382	hypothetical prote
294	54	11.7	248	1	PRMSC2	granzyme C (EC 3.4
295	54	11.7	259	2	C64481	conserved hypothet
296	54	11.7	292	2	T14627	hypothetical prote
297	54	11.7	316	2	F91044	transaldolase A [i
298	54	11.7	316	2	A85889	transaldolase A [i
299	54	11.7	316	2	G65021	transaldolase (EC
300	54	11.7	328	2	A69218	hypothetical prote
301	54	11.7	346	2	C86413	cysteine proteinas
302	54	11.7	351	2	I68620	rod outer segment
303	54	11.7	356	2	S66348	cysteine proteinas
304	54	11.7	356	2	B97742	hypothetical prote
305	54	11.7	359	2	F69061	hypothetical prote
306	54	11.7	386	2	A72313	hypothetical prote
307	54	11.7	394	2	C64185	cell division prot
308	54	11.7	428	2	S08084	gene IV protein -
309	54	11.7	440	2	E84118	UDP-N-acetylglucos
310	54	11.7	456	2	AH0551	proline-specific p
311	54	11.7	476	2	T40086	hypothetical prote
312	54	11.7	549	2	C86692	peptide-binding pr
313	54	11.7	558	2	AE1236	glycerol 3 phospha
314	54	11.7	573	1	S33212	INDA1 protein - fu
315	54	11.7	604	2	B84221	hypothetical prote
316	54	11.7	625	2	T25373	hypothetical prote
317	54	11.7	634	2	T33528	hypothetical prote
318	54	11.7	787	2	T38224	probable glycosyl
319	54	11.7	869	2	A96558	probable protein k
320	54	11.7	880	2	S49627	regulatory protein
321	54	11.7	885	2	G83260	aminopeptidase N P
322	54	11.7	909	2	T00009	probable primase (
323	54	11.7	967	2	I40889	sarcosine oxidase
324	54	11.7	993	2	A38437	probable homeotic
325	54	11.7	1072	2	T50949	verprolin related
326	54	11.7	1222	2	G72614	probable reverse g
327	54	11.7	1283	2	T18939	hypothetical prote
328	53.5	11.6	114	2	C90344	hypothetical prote
329	53.5	11.6	153	2	T49895	oleosin-like prote
330	53.5	11.6	173	2	S01145	hypothetical prote
331	53.5	11.6	211	2	G82573	CDP-diacylglycerol
332	53.5	11.6	225	1	CYFGE	epsilon-crystallin
333	53.5	11.6	269	2	D96957	uncharacterized me
334	53.5	11.6	282	2	PQ0388	cell fusion glycop
335	53.5	11.6	296	2	C90978	IS629 transposase
336	53.5	11.6	296	2	H85824	IS629 transposase
337	53.5	11.6	303	2	T13598	trypsin homolog -
338	53.5	11.6	307	2	B87292	conserved hypothet
339	53.5	11.6	339	2	H71265	hypothetical prote
340	53.5	11.6	346	2	D70558	probable cydB prot
341	53.5	11.6	357	2	F81679	chorismate synthas
342	53.5	11.6	376	2	AF1943	multidrug-efflux t
343	53.5	11.6	378	2	T34372	hypothetical prote
344	53.5	11.6	383	2	T48018	hypothetical prote
345	53.5	11.6	410	2	A48585	transcription fact
346	53.5	11.6	412	2	AH3274	macrolide-efflux p
347	53.5	11.6	461	2	T06936	photosystem II chl
348	53.5	11.6	495	2	I57680	potassium channel
349	53.5	11.6	495	2	A40090	potassium channel
350	53.5	11.6	495	2	B39113	potassium channel
351	53.5	11.6	529	2	H84049	hypothetical prote
352	53.5	11.6	539	2	T32693	hypothetical prote
353	53.5	11.6	546	2	S47300	gene F protein - r
354	53.5	11.6	553	1	VGNZMV	cell fusion glycop
355	53.5	11.6	556	2	T03114	tegument protein -
356	53.5	11.6	571	1	H65169	probable transport
357	53.5	11.6	571	2	D91206	probable cotranspo
358	53.5	11.6	571	2	F86052	probable cotranspo
359	53.5	11.6	594	2	T43246	amino acid transpo
360	53.5	11.6	597	2	AH2351	serine/threonine k
361	53.5	11.6	890	2	T35237	probable secreted
362	53.5	11.6	945	2	S30398	aminopeptidase N h
363	53.5	11.6	985	2	T10339	DNA-directed DNA p
364	53.5	11.6	1045	2	E90705	hypothetical prote
365	53.5	11.6	1045	2	H85555	hypothetical prote
366	53.5	11.6	1047	2	E64790	ybdE protein - Esc
367	53.5	11.6	1075	2	S76433	cation efflux syst
368	53.5	11.6	1175	2	S51005	protein-tyrosine-p
369	53.5	11.6	2037	2	T16881	hypothetical prote
370	53.5	11.6	3566	1	A40701	tenascin-X precurs
371	53	11.5	90	2	T33692	hypothetical prote
372	53	11.5	148	2	A84636	similar to avrRpt2
373	53	11.5	154	1	F70002	conserved hypothet
374	53	11.5	166	2	D58889	NADH2 dehydrogenas
375	53	11.5	201	2	A71124	hypothetical prote
376	53	11.5	202	2	JC6205	cell surface antig
377	53	11.5	210	2	JC5448	serine proteinase
378	53	11.5	214	2	AH0265	probable membrane
379	53	11.5	216	2	JC7930	small neutral amin
380	53	11.5	224	2	S67949	beta-tubulin ASL1
381	53	11.5	224	2	S73823	MG243 homolog H91_
382	53	11.5	257	2	D71544	hypothetical prote
383	53	11.5	264	2	A75076	membrane protein P
384	53	11.5	279	2	A95933	probable inositol
385	53	11.5	300	2	B83100	inhibitor of chrom
386	53	11.5	306	2	A88040	protein F47F6.1 [i
387	53	11.5	310	2	D87704	integral membrane
388	53	11.5	339	2	AG0165	L-allo-threonine a
389	53	11.5	342	2	A44965	cysteine proteinas
390	53	11.5	342	2	A45524	cysteine proteinas
391	53	11.5	364	2	AH1857	anthranilate phosp
392	53	11.5	376	2	E95879	probable sugar ABC
393	53	11.5	377	2	A53044	geranylgeranyl-dip
394	53	11.5	385	2	A91178	probable membrane

395	53	11.5	385	2	B86024	probable membrane
396	53	11.5	385	2	S47733	yhiU protein precu
397	53	11.5	386	2	A26017	patatin T5 precurs
398	53	11.5	403	2	E69873	cell-division prot
399	53	11.5	405	2	S61551	breast-regressing
400	53	11.5	409	2	F83493	probable MFS trans
401	53	11.5	418	2	H82087	NupC family protei
402	53	11.5	426	2	B82712	ATP-dependent Clp
403	53	11.5	438	2	G87675	arylesterase-relat
404	53	11.5	447	2	H86534	hypothetical prote
405	53	11.5	447	2	H72089	hypothetical prote
406	53	11.5	463	2	B81580	hypothetical prote
407	53	11.5	469	1	AJEBQT	glutamate-ammonia
408	53	11.5	469	2	AI0949	glutamine syntheta
409	53	11.5	469	2	S23899	glutamate-ammonia
410	53	11.5	471	2	S78347	photosystem II chl
411	53	11.5	515	2	B84406	TRK potassium upta
412	53	11.5	581	2	T38501	hypothetical prote
413	53	11.5	586	2	T20036	hypothetical prote
414	53	11.5	588	2	AC2276	oligopeptide bindi
415	53	11.5	605	2	E69153	cadmium efflux ATP
416	53	11.5	610	2	A55939	dihydrolipoamide S
417	53	11.5	618	2	AI3303	hypothetical prote
418	53	11.5	637	2	T49099	dihydrolipoamide S
419	53	11.5	653	2	A83154	probable choline t
420	53	11.5	656	2	T52064	dnaJ-like protein
421	53	11.5	728	2	D86278	hypothetical prote
422	53	11.5	770	2	T23999	hypothetical prote
423	53	11.5	776	2	T02584	probable protein k
424	53	11.5	1005	2	B82969	sarcosine oxidase
425	53	11.5	1070	2	JC4593	protein-tyrosine k
426	53	11.5	1162	2	E84431	probable Na+/H+ an
427	53	11.5	1176	2	I58345	protein tyrosine p
428	53	11.5	1240	1	DJBE21	DNA-directed DNA p
429	53	11.5	1250	2	T00454	hypothetical prote
430	53	11.5	1305	2	T23314	hypothetical prote
431	53	11.5	1326	2	B56395	secretory phosphol
432	53	11.5	1331	2	S05011	calcium channel al
433	53	11.5	1465	2	A56395	secretory phosphol
434	53	11.5	1529	2	T16779	hypothetical prote
435	53	11.5	2143	2	JH0427	voltage-dependent
436	53	11.5	2166	2	S11339	calcium channel pr
437	53	11.5	2171	2	S05054	calcium channel al
438	53	11.5	2599	2	A96616	unknown protein F1
439	52.5	11.4	71	2	I50439	vitellogenin III -
440	52.5	11.4	78	2	G64333	hypothetical prote
441	52.5	11.4	159	2	E85360	ribosomal protein
442	52.5	11.4	165	2	C72116	hypothetical prote
443	52.5	11.4	210	2	A83516	probable outer mem
444	52.5	11.4	219	2	F75402	probable competenc
445	52.5	11.4	219	2	AC1881	hypothetical prote
446	52.5	11.4	244	2	S29982	class II histocomp
447	52.5	11.4	245	2	S29980	class II histocomp
448	52.5	11.4	256	2	S14518	chlorophyll a/b-bi
449	52.5	11.4	257	2	S29981	class II histocomp
450	52.5	11.4	285	1	A43556	homeotic protein H
451	52.5	11.4	289	2	E64330	dihydrodipicolinat
452	52.5	11.4	296	2	S09261	probable transposa
453	52.5	11.4	301	2	B64189	glycine cleavage s
454	52.5	11.4	309	2	A87564	membrane protein,
455	52.5	11.4	310	2	C39778	tagatose-6-phospha
456	52.5	11.4	310	2	T31125	hypothetical prote
457	52.5	11.4	322	2	AF1031	hypothetical prote
458	52.5	11.4	332	2	C72310	conserved hypothet
459	52.5	11.4	334	2	D81217	hypothetical prote
460	52.5	11.4	334	2	T33950	hypothetical prote
461	52.5	11.4	342	2	C48435	cysteine proteinas
462	52.5	11.4	356	2	D84280	hypothetical prote
463	52.5	11.4	360	2	T51344	RNA helicase RH18
464	52.5	11.4	366	2	A49877	prostaglandin F re
465	52.5	11.4	377	2	C69758	amino acid transpo
466	52.5	11.4	394	2	B86507	hypothetical prote
467	52.5	11.4	394	2	B81554	hypothetical prote
468	52.5	11.4	409	2	T47644	protein phosphatas
469	52.5	11.4	410	2	B48585	transcription fact
470	52.5	11.4	421	2	T35515	hypothetical prote
471	52.5	11.4	422	2	JE0239	lin-10 protein - r
472	52.5	11.4	422	2	E82904	hypothetical prote
473	52.5	11.4	429	2	AF0681	probable voltage g
474	52.5	11.4	429	2	S30049	transcription fact
475	52.5	11.4	452	2	G95356	probable oxidoredu
476	52.5	11.4	500	2	H70629	probable AMINOPEPT
477	52.5	11.4	514	2	T21286	hypothetical prote
478	52.5	11.4	523	2	S53401	probable membrane
479	52.5	11.4	533	1	YRMSCS	monophenol monooxy
480	52.5	11.4	542	2	AH2191	hypothetical prote
481	52.5	11.4	542	2	AI3564	hypothetical membr
482	52.5	11.4	546	2	B32688	beta-galactosidase
483	52.5	11.4	549	2	G91178	cytoplasmic trehal
484	52.5	11.4	549	2	H86024	cytoplasmic trehal
485	52.5	11.4	549	2	S47739	probable alpha,alp
486	52.5	11.4	572	2	A55676	excitatory amino a
487	52.5	11.4	652	2	AH2245	thiamin biosynthes
488	52.5	11.4	657	1	A64079	2',3'-cyclic-nucle
489	52.5	11.4	686	2	T06700	hypothetical prote
490	52.5	11.4	699	2	T12170	NADH2 dehydrogenas
491	52.5	11.4	699	2	T12172	NADH2 dehydrogenas
492	52.5	11.4	699	2	T12173	NADH2 dehydrogenas
493	52.5	11.4	795	1	SYECFB	phenylalanine-tRNA
494	52.5	11.4	795	2	H85779	phenylalanine tRNA
495	52.5	11.4	795	2	D90931	phenylalanine tRNA
496	52.5	11.4	803	2	F83360	glucose dehydrogen
497	52.5	11.4	826	2	E90289	malate synthase, p
498	52.5	11.4	883	2	AE0207	conserved hypothet
499	52.5	11.4	977	2	T41289	hypothetical prote
500	52.5	11.4	1011	2	T40851	hypothetical prote
501	52.5	11.4	1205	2	T18517	procollagen N-endo
502	52.5	11.4	1225	1	S24284	E2 glycoprotein pr
503	52.5	11.4	1225	2	A36607	E2 glycoprotein -
504	52.5	11.4	1345	1	VCBEH6	major capsid prote
505	52.5	11.4	1453	2	S41453	spike protein - ca
506	52.5	11.4	1541	2	T30227	pipecolate-incorpo
507	52.5	11.4	1544	2	T29482	hypothetical prote
508	52.5	11.4	2285	1	G02434	DNA-directed DNA p
509	52	11.3	119	2	D64611	hypothetical prote
510	52	11.3	122	2	F75351	hypothetical prote
511	52	11.3	148	2	D64356	conserved hypothet
512	52	11.3	160	2	G95113	regulatory protein
513	52	11.3	160	2	H97982	regulatory protein
514	52	11.3	175	2	AE1508	hypothetical prote
515	52	11.3	202	2	JC4635	tumor-associated L
516	52	11.3	207	2	T45600	hypothetical prote
517	52	11.3	219	2	G97271	probable phosphogl
518	52	11.3	235	2	E82173	pseudouridine synt
519	52	11.3	238	2	C82866	conjugal transfer
520	52	11.3	260	2	I56559	neuropsin - mouse
521	52	11.3	262	2	B81200	conserved hypothet
522	52	11.3	265	2	D83761	hypothetical prote
523	52	11.3	291	2	B75618	chromosome partiti
524	52	11.3	295	2	E85661	probable transposa
525	52	11.3	297	2	T47857	myb protein-like -
526	52	11.3	310	2	S46239	ribosome-inactivat
527	52	11.3	310	2	T32006	hypothetical prote
528	52	11.3	320	2	AI2305	hypothetical prote
529	52	11.3	327	2	AH2608	transcription regu
530	52	11.3	327	2	G97390	araC family transc
531	52	11.3	359	2	A43532	B-cell surface ant
532	52	11.3	364	2	B71139	hypothetical prote
533	52	11.3	372	2	B64819	probable membrane
534	52	11.3	372	2	B85591	hypothetical prote
535	52	11.3	372	2	G90740	hypothetical prote
536	52	11.3	375	2	S47704	hypothetical 41.1K
537	52	11.3	375	2	F91173	probable transport
538	52	11.3	375	2	F86019	probable transport
539	52	11.3	379	2	F83152	hypothetical prote
540	52	11.3	397	2	B70048	conserved hypothet

541	52	11.3	417	2	E69804	multidrug resistan
542	52	11.3	457	2	S39079	puff C-8 protein -
543	52	11.3	469	2	D81017	chloride channel p
544	52	11.3	470	2	C70641	hypothetical prote
545	52	11.3	491	2	S75449	hypothetical prote
546	52	11.3	502	2	G87433	conserved hypothet
547	52	11.3	502	2	T29729	hypothetical prote
548	52	11.3	526	2	H85891	hydrogenase 4 memb
549	52	11.3	526	2	D91047	hydrogenase 4 memb
550	52	11.3	530	2	D87255	apolipoprotein N-a
551	52	11.3	534	2	T27054	hypothetical prote
552	52	11.3	544	2	T17422	halogenase-like pr
553	52	11.3	548	2	C82698	electron transfer
554	52	11.3	553	2	S75892	probable glycerol-
555	52	11.3	567	2	H87370	major facilitator
556	52	11.3	573	2	A33533	cell surface glyco
557	52	11.3	579	2	A64100	inner membrane cop
558	52	11.3	635	2	H69626	PTS fructose-speci
559	52	11.3	706	2	H81943	probable polyribon
560	52	11.3	707	2	C81161	polyribonucleotide
561	52	11.3	733	2	F82965	hypothetical prote
562	52	11.3	738	2	S37876	glutamine-rich pro
563	52	11.3	773	2	AH2061	hypothetical prote
564	52	11.3	823	2	A96737	hypothetical prote
565	52	11.3	840	2	T21333	hypothetical prote
566	52	11.3	869	2	A95156	conserved hypothet
567	52	11.3	878	2	D98022	conserved hypothet
568	52	11.3	906	2	AE2533	hypothetical prote
569	52	11.3	1016	2	T00375	hypothetical prote
570	52	11.3	1017	2	T37201	hypothetical prote
571	52	11.3	1106	2	A97647	cation efflux syst
572	52	11.3	1106	2	AG2870	Acr family transpo
573	52	11.3	1146	2	T09112	probable sensor ki
574	52	11.3	1146	2	A82174	sensory box sensor
575	52	11.3	1484	2	C97196	probable membrane
576	52	11.3	1957	2	S68453	sodium channel pro
577	52	11.3	2139	2	A44467	voltage-dependent
578	52	11.3	2220	2	A45290	calcium channel pr
579	52	11.3	3429	2	T13853	hypothetical prote
580	51.5	11.2	116	2	A83693	transcription regu
581	51.5	11.2	122	1	PSABA	phospholipase A2 (
582	51.5	11.2	131	2	C72563	hypothetical prote
583	51.5	11.2	146	2	S42570	flavodoxin - Desul
584	51.5	11.2	167	2	H86784	VPS29-like phospho
585	51.5	11.2	172	2	F75491	conserved hypothet
586	51.5	11.2	206	1	I40173	orotate phosphorib
587	51.5	11.2	209	2	T00733	hypothetical prote
588	51.5	11.2	212	1	A49436	dual specificity p
589	51.5	11.2	222	2	H64495	cobalamin biosynth
590	51.5	11.2	270	2	A29934	pancreatic elastas
591	51.5	11.2	276	2	A70425	hypothetical prote
592	51.5	11.2	282	2	AC2294	hypothetical prote
593	51.5	11.2	289	2	G97192	oligopeptide ABC-t
594	51.5	11.2	299	2	B95939	probable spermidin
595	51.5	11.2	299	2	H97884	hypothetical prote
596	51.5	11.2	312	2	B69170	UDP-N-acetylmuramy
597	51.5	11.2	313	2	S75329	hypothetical prote
598	51.5	11.2	314	2	T21971	hypothetical prote
599	51.5	11.2	319	2	T02691	glossy1 protein gl
600	51.5	11.2	342	2	T16806	hypothetical prote
601	51.5	11.2	355	2	S76667	hypothetical prote
602	51.5	11.2	364	2	G82734	acetylornithine de
603	51.5	11.2	366	2	I53488	prostaglandin F2 a
604	51.5	11.2	366	2	S51281	F2-alpha receptor
605	51.5	11.2	370	2	AH1485	fructose-specific
606	51.5	11.2	370	2	AI1124	fructose-specific
607	51.5	11.2	376	2	A75381	peptide ABC transp
608	51.5	11.2	380	2	D83174	probable acetylpol
609	51.5	11.2	381	2	A35300	G protein-coupled
610	51.5	11.2	381	2	F87553	aminotransferase,
611	51.5	11.2	382	2	G84971	ompF-like porin [i
612	51.5	11.2	383	2	I53870	Edg-1 orphan recep
613	51.5	11.2	390	2	C95954	hypothetical prote
614	51.5	11.2	410	2	S45894	regulatory protein
615	51.5	11.2	429	2	F87038	probable membrane
616	51.5	11.2	438	2	A83037	probable MFS trans
617	51.5	11.2	450	2	C96704	unknown protein, 2
618	51.5	11.2	451	2	F75177	tryptophan synthas
619	51.5	11.2	474	1	A40570	lipoprotein lipase
620	51.5	11.2	478	1	C42790	cystathionine beta
621	51.5	11.2	478	2	T30763	hypothetical prote
622	51.5	11.2	478	2	T32476	probable protein-t
623	51.5	11.2	481	2	B82130	pyruvate kinase II
624	51.5	11.2	493	2	T21445	hypothetical prote
625	51.5	11.2	509	2	G82409	glyceraldehyde 3-p
626	51.5	11.2	513	2	T34546	hypothetical prote
627	51.5	11.2	525	2	A70735	probable guaA prot
628	51.5	11.2	531	2	D96965	PTS system, arbuti
629	51.5	11.2	534	1	JU0274	cell fusion glycop
630	51.5	11.2	536	2	D81700	CTP synthase TC045
631	51.5	11.2	536	2	F85697	hypothetical prote
632	51.5	11.2	536	2	D64865	probable Na+/H+-ex
633	51.5	11.2	536	2	F90839	hypothetical prote
634	51.5	11.2	540	1	JU0470	site-specific DNA-
635	51.5	11.2	541	1	A70022	multidrug-efflux t
636	51.5	11.2	541	2	JN0511	heat shock protein
637	51.5	11.2	547	2	T46059	MAP kinase - Arabi
638	51.5	11.2	549	2	T51099	MAP kinase [import
639	51.5	11.2	550	1	E48556	cell fusion glycop
640	51.5	11.2	558	2	C72391	conserved hypothet
641	51.5	11.2	560	2	S27387	interferon alpha r
642	51.5	11.2	561	1	A42790	cystathionine beta
643	51.5	11.2	623	2	T35377	probable membrane
644	51.5	11.2	666	2	AF0815	transketolase (EC
645	51.5	11.2	667	1	A48660	transketolase (EC
646	51.5	11.2	667	2	G91044	transketolase 2 is
647	51.5	11.2	667	2	B85889	transketolase 2 is
648	51.5	11.2	682	2	T12715	NADH2 dehydrogenas
649	51.5	11.2	724	2	T19601	hypothetical prote
650	51.5	11.2	726	2	T31287	hypothetical prote
651	51.5	11.2	763	2	AI3443	Na+/H+ antiporter
652	51.5	11.2	765	2	B75288	hypothetical prote
653	51.5	11.2	795	2	AE0705	phenylalanyl-tRNA
654	51.5	11.2	829	2	T29372	hypothetical prote
655	51.5	11.2	846	2	T27282	hypothetical prote
656	51.5	11.2	869	2	C56617	cfaC protein precu
657	51.5	11.2	1451	1	JQ1719	E2 glycoprotein pr
658	51.5	11.2	1755	2	T51532	hypothetical prote
659	51.5	11.2	1784	2	T43167	sodium channel pro
660	51.5	11.2	2301	1	GNNYTN	genome polyprotein
661	51.5	11.2	2303	1	GNNYTM	genome polyprotein
662	51	11.1	89	2	AH3403	hypothetical prote
663	51	11.1	93	2	A86491	CT001 hypothetical
664	51	11.1	93	2	F72130	conserved hypothet
665	51	11.1	95	2	AG2439	hypothetical prote
666	51	11.1	97	2	C75415	hypothetical prote
667	51	11.1	106	2	A72588	hypothetical prote
668	51	11.1	152	2	H95153	conserved hypothet
669	51	11.1	173	2	AF2518	hypothetical prote
670	51	11.1	188	2	T15651	hypothetical prote
671	51	11.1	201	2	E75039	multiple antibioti
672	51	11.1	202	2	A81441	probable orotate p
673	51	11.1	204	2	A82389	conserved hypothet
674	51	11.1	212	2	I67437	cysteine proteinas
675	51	11.1	221	2	S75146	hypothetical prote
676	51	11.1	229	2	E85806	hypothetical prote
677	51	11.1	229	2	D90958	hypothetical prote
678	51	11.1	240	2	T02059	GTP-binding regula
679	51	11.1	246	2	S26826	histone H1 - maize
680	51	11.1	246	2	T28166	hypothetical prote
681	51	11.1	261	2	A71192	probable glucose 1
682	51	11.1	263	2	AG2280	glutathione S-tran
683	51	11.1	264	2	G96978	uncharacterized co
684	51	11.1	265	2	B81229	phosphatidate cyti
685	51	11.1	265	2	A82000	phosphatidate cyti
686	51	11.1	268	2	S03328	embryonic abundant

687	51	11.1	279	2	T22051	hypothetical prote
688	51	11.1	282	2	E64063	hypothetical prote
689	51	11.1	282	2	A41025	aspergillopepsin I
690	51	11.1	285	2	T15498	hypothetical prote
691	51	11.1	295	2	F90938	hypothetical prote
692	51	11.1	295	2	B85664	transposase for IS
693	51	11.1	295	2	D90801	hypothetical prote
694	51	11.1	295	2	B85613	probable transposa
695	51	11.1	309	2	AF0746	motility protein B
696	51	11.1	321	2	A55090	cathepsin O (EC 3.
697	51	11.1	328	1	S64306	hypothetical prote
698	51	11.1	348	2	AG0645	spermidine/putresc
699	51	11.1	355	2	E96785	protein F10A5.28 [
700	51	11.1	357	2	A71523	probable chorismat
701	51	11.1	361	2	A45211	prostaglandin E re
702	51	11.1	362	2	A53058	prostaglandin F2-a
703	51	11.1	364	2	S65009	prostaglandin E re
704	51	11.1	365	2	A42414	prostaglandin E re
705	51	11.1	372	2	S75587	H+/Ca2+ exchanging
706	51	11.1	375	2	T03256	GTP-binding protei
707	51	11.1	377	2	T04086	GTP binding protei
708	51	11.1	377	2	T16985	GTP-binding protei
709	51	11.1	379	2	AB2423	hypothetical prote
710	51	11.1	384	2	A69622	ferrichrome ABC tr
711	51	11.1	394	2	B85535	probable transport
712	51	11.1	394	2	F90684	probable transport
713	51	11.1	402	2	B82491	NupC family protei
714	51	11.1	404	2	T39270	conserved hypothet
715	51	11.1	409	2	G90491	conserved hypothet
716	51	11.1	416	2	T14554	calreticulin - bee
717	51	11.1	418	2	S31124	hypothetical prote
718	51	11.1	421	2	B82062	conserved hypothet
719	51	11.1	423	2	AB0054	probable Na+ depen
720	51	11.1	435	2	E71350	probable aspartate
721	51	11.1	439	2	S58327	cobalt accumulatio
722	51	11.1	439	2	T18898	hypothetical prote
723	51	11.1	440	2	AD1073	thymidine phosphor
724	51	11.1	449	2	C86496	hypothetical prote
725	51	11.1	449	2	D72127	hypothetical prote
726	51	11.1	449	2	A81544	hypothetical prote
727	51	11.1	450	2	AB1420	PTS cellobiose-spe
728	51	11.1	450	2	AC1795	PTS cellobiose-spe
729	51	11.1	458	1	YTBSY8	tetracycline resis
730	51	11.1	460	2	S06469	photosystem II chl
731	51	11.1	466	2	E84132	aminopeptidase BH3
732	51	11.1	468	2	A69468	ammonium transport
733	51	11.1	485	2	A72006	arginine/ornithine
734	51	11.1	514	2	A96671	Ammonium transport
735	51	11.1	516	2	T09859	cytochrome-c oxida
736	51	11.1	525	2	T00459	hypothetical prote
737	51	11.1	528	2	T22583	hypothetical prote
738	51	11.1	531	2	T12406	cytochrome-c oxida
739	51	11.1	560	2	T51485	sugar transporter-
740	51	11.1	616	2	T07611	aconitate hydratas
741	51	11.1	635	1	A64162	cytochrome c-type
742	51	11.1	639	2	JQ0607	glucan 1,4-alpha-g
743	51	11.1	699	2	A96802	unknown protein [i
744	51	11.1	745	1	A70458	phosphoribosylform
745	51	11.1	749	1	A39329	phospholipase A2 (
746	51	11.1	754	2	S37403	transcription fact
747	51	11.1	770	2	T50308	probable translati
748	51	11.1	778	2	E97224	ATP-dependent Lon
749	51	11.1	854	2	T23837	hypothetical prote
750	51	11.1	862	2	T46289	hypothetical prote
751	51	11.1	873	2	T16282	hypothetical prote
752	51	11.1	887	2	T01113	translation initia
753	51	11.1	967	2	A30325	membrane alanyl am
754	51	11.1	1075	2	D70568	hypothetical prote
755	51	11.1	1325	2	A64905	ydeK protein - Esc
756	51	11.1	1790	1	S27772	vitellogenin precu
757	50.5	11.0	137	2	D75337	hypothetical prote
758	50.5	11.0	141	2	E72580	hypothetical prote
759	50.5	11.0	155	2	T22027	hypothetical prote
760	50.5	11.0	173	2	S59864	TRAP-like protein
761	50.5	11.0	201	1	IMBPSB	immunity protein -
762	50.5	11.0	204	2	E83036	hypothetical prote
763	50.5	11.0	208	2	F71314	probable transcrip
764	50.5	11.0	217	2	I51062	MHC class II beta
765	50.5	11.0	224	2	T34686	probable integral
766	50.5	11.0	227	2	T12797	immunity protein d
767	50.5	11.0	228	2	C28551	hypothetical prote
768	50.5	11.0	231	2	H81698	hypothetical prote
769	50.5	11.0	233	2	JH0372	42K surface glycop
770	50.5	11.0	234	2	E95360	hypothetical prote
771	50.5	11.0	240	1	TQEC34	transposase - Esch
772	50.5	11.0	247	2	I51060	MHC class II beta
773	50.5	11.0	247	2	I51059	MHC class II beta
774	50.5	11.0	249	2	S75671	hypothetical prote
775	50.5	11.0	249	2	H95256	ABC transporter, p
776	50.5	11.0	250	2	T09160	proteasome subunit
777	50.5	11.0	252	2	F70711	probable membranep
778	50.5	11.0	253	2	A98122	hypothetical prote
779	50.5	11.0	255	2	JN0829	3alpha-hydroxyster
780	50.5	11.0	258	2	A69805	hypothetical prote
781	50.5	11.0	260	2	F82954	probable short-cha
782	50.5	11.0	264	2	D87504	hypothetical prote
783	50.5	11.0	286	2	E86844	shikimate 5-dehydr
784	50.5	11.0	288	2	F85818	hypothetical prote
785	50.5	11.0	293	2	A83623	hypothetical prote
786	50.5	11.0	296	2	A85841	probable transposa
787	50.5	11.0	296	2	D91284	hypothetical prote
788	50.5	11.0	296	2	F90868	hypothetical prote
789	50.5	11.0	296	2	D90995	hypothetical prote
790	50.5	11.0	296	2	E91020	hypothetical prote
791	50.5	11.0	296	2	A91132	hypothetical prote
792	50.5	11.0	296	2	F91111	hypothetical prote
793	50.5	11.0	296	2	G90998	hypothetical prote
794	50.5	11.0	296	2	T00240	transposase - Esch
795	50.5	11.0	296	2	B90837	hypothetical prote
796	50.5	11.0	296	2	C91065	hypothetical prote
797	50.5	11.0	296	2	H90779	hypothetical prote
798	50.5	11.0	296	2	C90906	hypothetical prote
799	50.5	11.0	296	2	A99972	hypothetical prote
800	50.5	11.0	297	2	T09542	endonuclease G (EC
801	50.5	11.0	297	2	T45436	hypothetical membr
802	50.5	11.0	302	2	S02728	actinidain (EC 3.4
803	50.5	11.0	302	2	S60955	probable membrane
804	50.5	11.0	313	2	AH1300	malonyl CoA-acyl c
805	50.5	11.0	314	2	F86928	34 kDa antigen [im
806	50.5	11.0	317	2	T27994	hypothetical prote
807	50.5	11.0	324	2	A86839	conserved hypothet
808	50.5	11.0	327	2	S61982	probable membrane
809	50.5	11.0	332	2	S77386	nitrate transport
810	50.5	11.0	346	2	C71390	NADH2 dehydrogenas
811	50.5	11.0	351	2	A69808	H+/Ca2+ exchanger
812	50.5	11.0	355	1	BVECMG	UDP-N-acetylglucos
813	50.5	11.0	355	2	F85491	hypothetical prote
814	50.5	11.0	355	2	F90640	hypothetical prote
815	50.5	11.0	361	2	F87286	cation efflux fami
816	50.5	11.0	362	2	JC7559	sphingosine 1-phos
817	50.5	11.0	364	2	H70776	hypothetical prote
818	50.5	11.0	377	2	B53044	geranylgeranyl-dip
819	50.5	11.0	379	2	T45768	protein phosphatas
820	50.5	11.0	382	2	H90500	glycolate oxidase
821	50.5	11.0	398	2	S75202	hypothetical prote
822	50.5	11.0	399	2	T26257	hypothetical prote
823	50.5	11.0	406	2	T27947	hypothetical prote
824	50.5	11.0	407	2	E70309	hypothetical prote
825	50.5	11.0	408	2	T29949	hypothetical prote
826	50.5	11.0	410	2	JC7584	basic helix-loop-h
827	50.5	11.0	411	2	AG3003	conserved hypothet
828	50.5	11.0	411	2	B98280	hypothetical prote
829	50.5	11.0	421	2	D70868	probable lipQ prot
830	50.5	11.0	424	2	A71846	glycinamide ribonu
831	50.5	11.0	424	2	B64672	glycinamide ribonu
832	50.5	11.0	441	2	AF0411	probable chloride

833	50.5	11.0	442	2	S56057	heavy metal ion re
834	50.5	11.0	448	2	A83775	hypothetical prote
835	50.5	11.0	460	2	G85525	probable deaminase
836	50.5	11.0	460	2	E90675	probable deaminase
837	50.5	11.0	470	2	T20851	hypothetical prote
838	50.5	11.0	471	2	D83546	probable amino aci
839	50.5	11.0	474	1	JH0790	lipoprotein lipase
840	50.5	11.0	507	2	T27627	hypothetical prote
841	50.5	11.0	509	2	G81929	probable iron-upta
842	50.5	11.0	510	2	T20850	hypothetical prote
843	50.5	11.0	515	2	G75267	ABC transporter, p
844	50.5	11.0	517	2	S21042	cytochrome-c oxida
845	50.5	11.0	518	2	S34565	gene G protein - h
846	50.5	11.0	518	2	F70831	probable PPE prote
847	50.5	11.0	520	2	AD2383	Na+/H+-exchanging
848	50.5	11.0	526	2	G83436	hypothetical prote
849	50.5	11.0	529	1	YRHU1	monophenol monooxy
850	50.5	11.0	543	2	T37570	WD repeat protein
851	50.5	11.0	543	2	S65462	glucose transport
852	50.5	11.0	544	2	AD1979	permease protein o
853	50.5	11.0	545	2	AC1914	hypothetical prote
854	50.5	11.0	546	2	B40407	sterol carrier pro
855	50.5	11.0	563	2	S32156	mandelonitrile lya
856	50.5	11.0	577	2	T52608	probable nitrate t
857	50.5	11.0	584	2	S40013	hypothetical prote
858	50.5	11.0	586	2	F84663	probable nitrate t
859	50.5	11.0	595	2	AH2718	aspartyl-tRNA synt
860	50.5	11.0	595	2	D97500	aspartyl)-tRNA syn
861	50.5	11.0	608	2	S76192	hypothetical prote
862	50.5	11.0	684	2	T25603	hypothetical prote
863	50.5	11.0	688	2	H96681	protein F1E22.10 [
864	50.5	11.0	704	2	F87706	prolyl oligopeptid
865	50.5	11.0	712	2	AD2721	H+ translocating p
866	50.5	11.0	714	2	H97502	h+ translocating p
867	50.5	11.0	731	2	E82922	phosphate transpor
868	50.5	11.0	736	2	AC2821	bacteriophytochrom
869	50.5	11.0	745	2	C97599	cyanobacterial phy
870	50.5	11.0	819	2	F87708	cell division prot
871	50.5	11.0	827	2	A95877	hypothetical prote
872	50.5	11.0	908	2	AI0327	two-component regu
873	50.5	11.0	942	1	JQ1674	protein kinase TMK
874	50.5	11.0	962	2	T05845	hypothetical prote
875	50.5	11.0	1163	1	RWHU1C	cell surface glyco
876	50.5	11.0	1188	2	T20333	hypothetical prote
877	50.5	11.0	1265	2	T47626	structural mainten
878	50.5	11.0	1317	2	T03748	apoptosis associat
879	50.5	11.0	1345	2	T44204	capsid protein U57
880	50.5	11.0	1345	2	T44017	major capsid prote
881	50.5	11.0	1400	2	B70963	hypothetical prote
882	50.5	11.0	1447	1	VGIHE3	E2 glycoprotein pr
883	50.5	11.0	1447	1	VGIHE2	E2 glycoprotein pr
884	50.5	11.0	1449	1	A43573	E2 glycoprotein pr
885	50.5	11.0	1449	1	VGIHFS	E2 glycoprotein pr
886	50.5	11.0	1577	2	T15851	hypothetical prote
887	50.5	11.0	1672	2	C81675	polymorphic membra
888	50.5	11.0	1921	2	T13827	kinesin-73 - fruit
889	50	10.8	89	2	H83795	hypothetical prote
890	50	10.8	100	2	AI2298	cobalt transport p
891	50	10.8	102	2	A75417	hypothetical prote
892	50	10.8	121	2	B72546	hypothetical prote
893	50	10.8	138	2	JC1342	phospholipase A2 (
894	50	10.8	147	2	S70109	hypothetical prote
895	50	10.8	150	2	G72660	hypothetical prote
896	50	10.8	170	2	B86842	hypothetical prote
897	50	10.8	175	2	T11179	NADH2 dehydrogenas
898	50	10.8	175	2	AE1149	hypothetical prote
899	50	10.8	186	2	E82625	outer membrane pro
900	50	10.8	195	2	T39603	BAG-family molecul
901	50	10.8	203	2	D81934	probable periplasm
902	50	10.8	203	2	F81171	cryptic protein NM
903	50	10.8	211	2	A47686	bacteriorhodopsin-
904	50	10.8	211	2	AC0268	probable exported
905	50	10.8	213	2	G75521	ABC transporter, A
906	50	10.8	214	2	T10737	extensin-like cell
907	50	10.8	216	2	AI1441	hypothetical prote
908	50	10.8	219	2	T38019	uracil phosphoribo
909	50	10.8	232	2	S29001	G protein-coupled
910	50	10.8	236	2	T32473	hypothetical prote
911	50	10.8	238	2	B64509	hypothetical prote
912	50	10.8	250	2	S51206	cruxrhodopsin-1 -
913	50	10.8	255	2	A71351	probable cobalt AB
914	50	10.8	256	2	A81277	probable oxidoredu
915	50	10.8	259	2	C75151	oxidoreductase PAB
916	50	10.8	265	2	D81315	hypothetical prote
917	50	10.8	265	2	G97460	hypothetical prote
918	50	10.8	268	2	C83369	probable binding p
919	50	10.8	274	2	E75614	conserved hypothet
920	50	10.8	293	2	T36063	probable integral
921	50	10.8	295	2	B85787	probable transposa
922	50	10.8	295	2	T00315	transposase - Esch
923	50	10.8	296	2	I67971	transposase - Esch
924	50	10.8	296	2	D90398	conserved hypothet
925	50	10.8	299	2	S50803	hypothetical prote
926	50	10.8	304	2	A72596	hypothetical prote
927	50	10.8	308	2	S22928	ubiquinol-cytochro
928	50	10.8	314	2	S72525	pectinesterase (EC
929	50	10.8	317	2	B87666	homoserine kinase
930	50	10.8	332	2	C87426	cysteine synthase
931	50	10.8	332	2	C84061	ferrichrome ABC tr
932	50	10.8	333	2	T36036	probable integral
933	50	10.8	337	2	AG0802	probable semialdeh
934	50	10.8	341	2	D48435	cysteine proteinas
935	50	10.8	348	2	E86818	dehydrogenase [imp
936	50	10.8	357	2	D83685	nicotinate-nucleot
937	50	10.8	357	2	T09261	JUN kinase-activat
938	50	10.8	372	2	S20056	para-hydroxybenzoa
939	50	10.8	375	2	T25089	hypothetical prote
940	50	10.8	380	2	A71390	ubiquinol-cytochro
941	50	10.8	388	2	D69468	ammonium transport
942	50	10.8	388	2	AF0183	probable exported
943	50	10.8	393	2	S61659	KTR1 protein - yea
944	50	10.8	397	2	E91296	probable thymidine
945	50	10.8	407	2	F70318	hypothetical prote
946	50	10.8	407	2	G75268	hypothetical prote
947	50	10.8	414	1	E70708	cytochrome P450 Rv
948	50	10.8	420	2	A82856	conserved hypothet
949	50	10.8	434	2	AI2379	hypothetical prote
950	50	10.8	435	2	G86907	D-alanyl-D-alanine
951	50	10.8	440	1	S56606	thymidine phosphor
952	50	10.8	440	2	G86137	thymidine phosphor
953	50	10.8	449	2	H69862	Na+-transporting A
954	50	10.8	457	1	A28468	chromogranin A pre
955	50	10.8	457	2	A53669	streptogrisin C (E
956	50	10.8	460	2	JL0145	interleukin-6 rece
957	50	10.8	473	1	F2RZ44	photosystem II chl
958	50	10.8	473	1	F2SP44	photosystem II chl
959	50	10.8	473	2	T08998	photosystem II pro
960	50	10.8	476	2	AC2306	hypothetical prote
961	50	10.8	489	2	AI1639	multidrug-efflux t
962	50	10.8	494	2	C70940	probable cobQ prot
963	50	10.8	498	2	F98149	hypothetical prote
964	50	10.8	514	2	C49507	potassium channel
965	50	10.8	516	2	S39686	Na+-dependent symp
966	50	10.8	532	2	JC1392	monophenol monooxy
967	50	10.8	533	2	AE3138	hypothetical prote
968	50	10.8	538	2	C83284	probable biotin-de
969	50	10.8	538	2	C86976	PPE-family protein
970	50	10.8	539	2	C83758	cephalosporin acyl
971	50	10.8	542	2	S50361	probable membrane
972	50	10.8	545	2	T18694	hypothetical prote
973	50	10.8	545	2	T39499	conserved hypothet
974	50	10.8	573	2	D83440	probable sulfate t
975	50	10.8	588	2	T25248	hypothetical prote
976	50	10.8	598	2	S66669	potassium channel
977	50	10.8	602	2	A49507	potassium channel
978	50	10.8	602	2	JH0166	potassium voltage-

979	50	10.8	606	2	S57552	hypothetical prote
980	50	10.8	613	2	A56031	potassium channel
981	50	10.8	614	2	E86194	hypothetical prote
982	50	10.8	700	2	B81266	DNA topoisomerase
983	50	10.8	749	1	B39898	phospholipase A2 (
984	50	10.8	756	2	C84682	hypothetical prote
985	50	10.8	789	2	AE2688	Na+/H+ antiporter
986	50	10.8	789	2	H97469	probable NADH dehy
987	50	10.8	810	1	P2WMBB	2a protein - broad
988	50	10.8	828	2	JC5807	trp3 protein - rat
989	50	10.8	835	2	F70363	cation transportin
990	50	10.8	836	2	C97525	clpA protein (AJ22
991	50	10.8	836	2	AD2744	ATP-dependent Clp
992	50	10.8	876	2	T07101	lipoxygenase (EC 1
993	50	10.8	993	2	F97717	hypothetical prote
994	50	10.8	1015	2	T15830	hypothetical prote
995	50	10.8	1021	2	A86421	Receptor-like seri
996	50	10.8	1022	2	F87635	AcrB/AcrD/AcrF fam
997	50	10.8	1277	2	T14152	synaptic scaffoldi
998	50	10.8	1338	2	T40993	protein kinase cek
999	50	10.8	1381	2	T31083	paranodin - rat
1000	50	10.8	1479	2	T42710	mannose receptor,
1001	50	10.8	1498	2	B97355	DNA segregation AT
1002	50	10.8	1505	2	S26765	genome polyprotein
1003	50	10.8	1524	2	S68553	surface layer prot
1004	50	10.8	1526	2	A96528	protein F27J15.14
1005	50	10.8	1687	2	S41742	calcium channel al
1006	50	10.8	2109	2	T31352	hypothetical prote
1007	50	10.8	2819	2	A90551	conserved hypothet
1008	49.5	10.7	63	2	B90031	hypothetical prote
1009	49.5	10.7	119	2	PH1544	Ig H chain V regio
1010	49.5	10.7	130	2	AD2901	hypothetical prote
1011	49.5	10.7	130	2	S67024	probable membrane
1012	49.5	10.7	150	2	F87507	conserved hypothet
1013	49.5	10.7	160	2	C35542	ribosomal protein
1014	49.5	10.7	165	2	F97676	succinate dehydrog
1015	49.5	10.7	165	2	S50195	oleosin - rape
1016	49.5	10.7	171	2	S22194	hypothetical prote
1017	49.5	10.7	172	2	I39644	apxIC protein - Ac
1018	49.5	10.7	197	2	AB2056	hypothetical prote
1019	49.5	10.7	214	2	D83881	siderophore (surfa
1020	49.5	10.7	218	2	AC1253	glycine betaine/ca
1021	49.5	10.7	218	2	AI1615	glycine betaine/ca
1022	49.5	10.7	226	2	F87449	cell division prot
1023	49.5	10.7	244	2	E84885	hypothetical prote
1024	49.5	10.7	251	2	AF2281	hypothetical prote
1025	49.5	10.7	252	1	A34702	amphiregulin precu
1026	49.5	10.7	255	2	H81302	probable membrane
1027	49.5	10.7	275	2	H90251	maltose transport
1028	49.5	10.7	294	2	B83040	ribosomal protein
1029	49.5	10.7	295	2	T04483	probable ring fing
1030	49.5	10.7	301	1	S10456	cytochrome c-type
1031	49.5	10.7	302	2	F83392	hypothetical prote
1032	49.5	10.7	305	2	AI0847	Iron transport pro
1033	49.5	10.7	313	2	AH1672	malonyl CoA-acyl c
1034	49.5	10.7	315	2	B98226	hypothetical prote
1035	49.5	10.7	315	2	AF3060	conserved hypothet
1036	49.5	10.7	327	2	T32164	hypothetical prote
1037	49.5	10.7	328	2	AD1916	alcohol dehydrogen
1038	49.5	10.7	330	2	H75353	probable nosX prot
1039	49.5	10.7	332	2	T33799	hypothetical prote
1040	49.5	10.7	334	2	T23444	hypothetical prote
1041	49.5	10.7	341	2	C98304	probable oligopept
1042	49.5	10.7	341	2	AB2979	hypothetical prote
1043	49.5	10.7	348	2	B48435	cysteine proteinas
1044	49.5	10.7	360	2	B87286	conserved hypothet
1045	49.5	10.7	367	2	C69500	group II decarboxy
1046	49.5	10.7	368	1	QQBEHG	early nuclear anti
1047	49.5	10.7	372	1	D69442	conserved hypothet
1048	49.5	10.7	374	1	I39857	spore germination
1049	49.5	10.7	374	2	T21513	hypothetical prote
1050	49.5	10.7	380	1	TAGB	actinidain (EC 3.4
1051	49.5	10.7	391	2	T43987	pp41, pol processi
1052	49.5	10.7	400	2	T46383	hypothetical prote
1053	49.5	10.7	401	2	D83022	hypothetical prote
1054	49.5	10.7	403	2	T09322	DNA polymerase pro
1055	49.5	10.7	424	2	D75330	probable beta-lact
1056	49.5	10.7	427	2	A49518	kallistatin precur
1057	49.5	10.7	430	1	S32570	malC protein - Str
1058	49.5	10.7	430	2	AF1356	hypothetical prote
1059	49.5	10.7	430	2	AG1726	hypothetical prote
1060	49.5	10.7	432	2	H64383	Na+ transporter -
1061	49.5	10.7	443	2	AE0309	probable sugar tra
1062	49.5	10.7	469	2	T34645	hypothetical prote
1063	49.5	10.7	469	2	S74825	probable Rieske ir
1064	49.5	10.7	476	1	VMUT4R	variant surface gl
1065	49.5	10.7	476	2	B86829	multidrug transpor
1066	49.5	10.7	478	2	T33942	hypothetical prote
1067	49.5	10.7	502	2	T26256	hypothetical prote
1068	49.5	10.7	505	2	G90419	metabolite permeas
1069	49.5	10.7	508	2	H86474	hypothetical prote
1070	49.5	10.7	514	2	F87592	hypothetical prote
1071	49.5	10.7	524	2	F85429	actin interacting
1072	49.5	10.7	538	2	T40298	membrane transport
1073	49.5	10.7	538	2	A83018	probable sodium/hy
1074	49.5	10.7	552	2	A51027	L-ascorbate oxidas
1075	49.5	10.7	553	2	B90153	2-isopropylmalate
1076	49.5	10.7	556	2	T46842	K+-transporting AT
1077	49.5	10.7	557	2	H97351	K+-transporting AT
1078	49.5	10.7	559	2	C87307	hypothetical prote
1079	49.5	10.7	566	2	B82173	probable ABC trans
1080	49.5	10.7	579	2	S11027	L-ascorbate oxidas
1081	49.5	10.7	583	2	T48473	amino acid transpo
1082	49.5	10.7	583	2	E83794	ABC transporter (A
1083	49.5	10.7	586	1	E69314	replication licens
1084	49.5	10.7	660	2	B97853	NADH2 dehydrogenas
1085	49.5	10.7	686	2	E71895	probable heavy-met
1086	49.5	10.7	697	2	T13670	NADH2 dehydrogenas
1087	49.5	10.7	698	2	T12625	NADH2 dehydrogenas
1088	49.5	10.7	699	2	T12673	NADH2 dehydrogenas
1089	49.5	10.7	700	2	T23629	hypothetical prote
1090	49.5	10.7	701	2	T13056	NADH2 dehydrogenas
1091	49.5	10.7	701	2	T13587	NADH2 dehydrogenas
1092	49.5	10.7	702	2	T13058	NADH2 dehydrogenas
1093	49.5	10.7	702	2	T12624	NADH2 dehydrogenas
1094	49.5	10.7	702	2	T13409	NADH2 dehydrogenas
1095	49.5	10.7	703	2	T13074	NADH2 dehydrogenas
1096	49.5	10.7	703	2	T13696	NADH2 dehydrogenas
1097	49.5	10.7	706	2	T12748	NADH2 dehydrogenas
1098	49.5	10.7	721	2	F82198	probable toxin sec
1099	49.5	10.7	732	2	A83481	probable TonB-depe
1100	49.5	10.7	734	1	DERZN5	NADH2 dehydrogenas
1101	49.5	10.7	738	2	S58612	NADH2 dehydrogenas
1102	49.5	10.7	740	2	B84741	hypothetical prote
1103	49.5	10.7	745	2	B84673	hypothetical prote
1104	49.5	10.7	753	2	F69338	pyruvate, water di
1105	49.5	10.7	770	2	B56695	transducin-like en
1106	49.5	10.7	776	2	S45495	isp4 protein - fis
1107	49.5	10.7	788	1	I59282	diacylglycerol kin
1108	49.5	10.7	795	2	D82225	phenylalanyl-tRNA
1109	49.5	10.7	822	2	T25866	hypothetical prote
1110	49.5	10.7	826	2	AC0086	outer membrane ush
1111	49.5	10.7	850	2	JC5700	ErbB kinase activa
1112	49.5	10.7	875	2	T12794	hypothetical yomG
1113	49.5	10.7	888	2	A54280	cell differentiati
1114	49.5	10.7	914	1	JN0550	iodide peroxidase
1115	49.5	10.7	945	2	S77052	cation-transportin
1116	49.5	10.7	1039	2	T38447	tetratricopeptide
1117	49.5	10.7	1069	2	D85383	hypothetical prote
1118	49.5	10.7	1084	2	T15616	hypothetical prote
1119	49.5	10.7	1121	2	JC7329	WD-repeat protein
1120	49.5	10.7	1132	2	T31107	telomerase reverse
1121	49.5	10.7	1163	2	A56097	arylphorin-binding
1122	49.5	10.7	1195	2	S76592	5-methyltetrahydro
1123	49.5	10.7	1354	2	AG0538	Rhs-family protein
1124	49.5	10.7	1461	2	E90696	hypothetical prote

1125	49.5	10.7	1461	2	A85547	hypothetical prote
1126	49.5	10.7	1492	2	A39322	cystic fibrosis tr
1127	49.5	10.7	2150	2	T08165	RNA1 polyprotein -
1128	49.5	10.7	2222	1	A36028	DNA-directed DNA p
1129	49.5	10.7	2403	2	T30875	PRP8 protein homol
1130	49.5	10.7	2500	1	WMHUE2	HIV-EP2 enhancer-b
1131	49.5	10.7	3655	2	T38084	TRAP-like protein
1132	49	10.6	98	2	T17363	NADH2 dehydrogenas
1133	49	10.6	98	2	T17177	NADH2 dehydrogenas
1134	49	10.6	99	2	D75182	lsu ribosomal prot
1135	49	10.6	129	2	T28983	hypothetical prote
1136	49	10.6	135	2	F86053	hypothetical prote
1137	49	10.6	135	2	D91207	hypothetical prote
1138	49	10.6	135	2	A65171	o135 protein - Esc
1139	49	10.6	137	1	JC4877	phospholipase A2 h
1140	49	10.6	140	2	S74898	hypothetical prote
1141	49	10.6	146	2	T06471	core protein - gar
1142	49	10.6	154	2	C71379	probable ATPase, c
1143	49	10.6	157	2	S18651	variant surface an
1144	49	10.6	157	2	S58025	probable olfactory
1145	49	10.6	159	2	S77852	probable phenylala
1146	49	10.6	160	2	S73261	plastoquinol-plast
1147	49	10.6	163	2	D71062	hypothetical prote
1148	49	10.6	166	2	D82909	hypothetical prote
1149	49	10.6	167	2	T11439	NADH2 dehydrogenas
1150	49	10.6	167	2	B71553	hypothetical prote
1151	49	10.6	167	2	AE3204	hypothetical prote
1152	49	10.6	169	2	B75490	hypothetical prote
1153	49	10.6	170	2	H71937	3-dehydroquinate d
1154	49	10.6	170	2	F90050	hypothetical prote
1155	49	10.6	172	2	T32259	hypothetical prote
1156	49	10.6	174	2	E90617	NADH dehydrogenase
1157	49	10.6	179	1	ERAD34	early E3 20.1K gly
1158	49	10.6	181	2	JX0247	serine proteinase
1159	49	10.6	185	2	T41299	hypothetical metal
1160	49	10.6	195	2	AF2690	conserved hypothet
1161	49	10.6	195	2	B97472	hypothetical prote
1162	49	10.6	196	2	T49023	hypothetical prote
1163	49	10.6	196	2	G87510	hypothetical prote
1164	49	10.6	203	2	E72345	endopeptidase Clp
1165	49	10.6	203	2	T32745	hypothetical prote
1166	49	10.6	205	2	T14744	hypothetical prote
1167	49	10.6	207	2	D75341	conserved hypothet
1168	49	10.6	212	2	AC0074	probable tellurium
1169	49	10.6	217	2	B90765	hypothetical prote
1170	49	10.6	224	2	AG1795	hypothetical prote
1171	49	10.6	236	2	E81406	hypothetical prote
1172	49	10.6	244	2	S07398	gamma-gliadin B pr
1173	49	10.6	255	4	S31866	Ig gamma-1 chain C
1174	49	10.6	262	2	T48546	hypothetical prote
1175	49	10.6	263	2	AB2559	transposase all806
1176	49	10.6	276	2	S73410	hypothetical prote
1177	49	10.6	287	2	E83928	transcription regu
1178	49	10.6	288	2	AH0247	probable binding-p
1179	49	10.6	300	2	G75436	conserved hypothet
1180	49	10.6	308	1	QRECMB	chemotaxis protein
1181	49	10.6	308	2	C85802	hypothetical prote
1182	49	10.6	308	2	G90953	chemotaxis protein
1183	49	10.6	308	2	H82936	hpr serine/threoni
1184	49	10.6	312	2	F87335	conserved hypothet
1185	49	10.6	322	2	AI2671	homoserine kinase
1186	49	10.6	322	2	G97453	homoserine kinase
1187	49	10.6	324	1	JC4280	carbonyl reductase
1188	49	10.6	334	2	T16772	hypothetical prote
1189	49	10.6	334	2	E87448	arginine N-succiny
1190	49	10.6	335	2	T40292	glyceraldehyde 3-p
1191	49	10.6	337	1	QQECH3	probable dehydroge
1192	49	10.6	337	2	C91029	probable PTS syste
1193	49	10.6	337	2	D85873	probable PTS syste
1194	49	10.6	345	2	T28026	hypothetical prote
1195	49	10.6	349	2	C86662	hypothetical prote
1196	49	10.6	352	2	A43113	chemokine (C-C) re
1197	49	10.6	353	2	H88939	protein C05E4.13 [
1198	49	10.6	355	2	S41686	geranylgeranyltran
1199	49	10.6	366	2	A64950	membrane-bound pen
1200	49	10.6	366	2	C85800	probable cytochrom
1201	49	10.6	366	2	G90951	probable cytochrom
1202	49	10.6	367	2	G96770	hypothetical prote
1203	49	10.6	370	2	AB0602	probable membrane
1204	49	10.6	378	2	F64446	chorismate synthas
1205	49	10.6	379	2	E69332	heterodisulfide re
1206	49	10.6	380	2	T11033	ubiquinol-cytochro
1207	49	10.6	382	2	AH2056	hypothetical prote
1208	49	10.6	385	2	A86227	hypothetical prote
1209	49	10.6	391	2	T39673	probable mannosylt
1210	49	10.6	396	2	T35024	probable glutathio
1211	49	10.6	400	2	C83511	flagellar protein
1212	49	10.6	404	2	B86962	probable secreted
1213	49	10.6	408	2	A37813	UDP-N-acetylglucos
1214	49	10.6	411	2	S75327	lysostaphin - Syne
1215	49	10.6	419	1	S47692	hypothetical 43.8K
1216	49	10.6	419	2	B91169	probable transport
1217	49	10.6	419	2	B86015	probable transport
1218	49	10.6	419	2	G70602	hypothetical prote
1219	49	10.6	425	2	A64977	hypothetical prote
1220	49	10.6	429	2	B87299	transporter, proba
1221	49	10.6	431	1	E70699	probable pknA prot
1222	49	10.6	439	2	D72716	hypothetical prote
1223	49	10.6	441	2	B82023	probable membrane-
1224	49	10.6	444	2	T24076	hypothetical prote
1225	49	10.6	448	2	A70398	cell division prot
1226	49	10.6	450	2	E69934	conserved hypothet
1227	49	10.6	458	2	AC1173	amino acid transpo
1228	49	10.6	458	2	AD1530	amino acid transpo
1229	49	10.6	463	2	C86042	probable transport
1230	49	10.6	463	2	B91195	probable transport
1231	49	10.6	463	2	H65166	probable transport
1232	49	10.6	463	2	H69822	sodium-glutamate s
1233	49	10.6	466	2	G72603	nitrate reductase
1234	49	10.6	469	1	AJECQ	glutamate-ammonia
1235	49	10.6	469	2	A83356	hypothetical prote
1236	49	10.6	469	2	G86074	glutamine syntheta
1237	49	10.6	469	2	H91227	glutamine syntheta
1238	49	10.6	473	2	T07548	photosystem II chl
1239	49	10.6	475	2	T36342	probable glutamate
1240	49	10.6	475	2	T06061	cellulase (EC 3.2.
1241	49	10.6	476	2	H96802	probable amino aci
1242	49	10.6	485	2	G65051	phosphotransferase
1243	49	10.6	485	2	C91075	hypothetical prote
1244	49	10.6	485	2	B85920	hypothetical prote
1245	49	10.6	491	2	B71957	ATP-dependent RNA
1246	49	10.6	492	2	G64550	ATP-dependent RNA
1247	49	10.6	493	2	AI1224	uroporphyrinogen-I
1248	49	10.6	493	2	AC1578	uroporphyrinogen-I
1249	49	10.6	495	1	A26396	T-cell surface gly
1250	49	10.6	496	2	F83124	probable transcrip
1251	49	10.6	507	2	JG0165	LAT1 protein - hum
1252	49	10.6	510	2	S55124	probable membrane
1253	49	10.6	515	2	C58892	cytochrome-c oxida
1254	49	10.6	516	2	T09949	cytochrome-c oxida
1255	49	10.6	522	1	IKECl	colicin E1 - Esche
1256	49	10.6	526	2	E65024	Hydrogenase-4 comp
1257	49	10.6	535	2	D96586	hypothetical prote
1258	49	10.6	542	2	C70732	probable integral
1259	49	10.6	553	1	H70786	probable dihydroli
1260	49	10.6	555	2	S27163	alpha,alpha-trehal
1261	49	10.6	557	2	AE3040	urocanase [importe
1262	49	10.6	563	2	G98245	hutu gene homolog
1263	49	10.6	573	2	S28901	glutamate transpor
1264	49	10.6	582	2	S22195	bps2 protein - Des
1265	49	10.6	586	2	PC6006	scaffolding protei
1266	49	10.6	597	2	S51212	BAK5 protein - bov
1267	49	10.6	602	2	E70067	conserved hypothet
1268	49	10.6	605	2	D83007	regulatory protein
1269	49	10.6	616	2	AG2957	hypothetical prote
1270	49	10.6	616	2	G98325	probable c4-dicarb

1271	49	10.6	618	2	F84409	arsenite transport
1272	49	10.6	629	2	S29685	retroviral recepto
1273	49	10.6	642	2	C84944	threonine-tRNA lig
1274	49	10.6	660	2	T09537	xanthophyll epoxid
1275	49	10.6	672	2	A65024	Hydrogenase-4 comp
1276	49	10.6	672	2	D85891	hydrogenase 4 memb
1277	49	10.6	672	2	H91046	hydrogenase 4 memb
1278	49	10.6	680	2	T29871	hypothetical prote
1279	49	10.6	719	2	S63392	probable membrane
1280	49	10.6	740	2	T03847	Fas-binding protei
1281	49	10.6	748	1	I50699	cytosolic phosphol
1282	49	10.6	784	2	JH0101	apolipoprotein B-1
1283	49	10.6	796	2	E87636	TonB-dependent rec
1284	49	10.6	799	2	T48690	hypothetical prote
1285	49	10.6	812	2	AG3138	fimbrial usher pro
1286	49	10.6	812	2	D98149	hypothetical prote
1287	49	10.6	816	2	T21713	hypothetical prote
1288	49	10.6	839	2	S35319	nucleoporin-intera
1289	49	10.6	862	2	S64821	probable membrane
1290	49	10.6	952	2	E84534	hypothetical prote
1291	49	10.6	969	2	F71418	hypothetical prote
1292	49	10.6	975	2	T22788	hypothetical prote
1293	49	10.6	976	2	S40697	processing endopro
1294	49	10.6	1041	2	B81281	probable secreted
1295	49	10.6	1054	2	T30933	chitinase (EC 3.2.
1296	49	10.6	1073	1	OYHUHX	heat-stable entero
1297	49	10.6	1086	2	T40354	hypothetical prote
1298	49	10.6	1190	2	T00842	probable histidine
1299	49	10.6	1207	2	T52459	sensory transducti
1300	49	10.6	1230	2	S47466	cellulose 1,4-beta
1301	49	10.6	1265	2	T51314	probable CO-induce
1302	49	10.6	1396	2	S36851	L-shaped tail fibe
1303	49	10.6	1430	2	AF0351	probable autotrans
1304	49	10.6	1530	2	E82085	glutamate synthase
1305	49	10.6	1648	2	F84833	probable SNF2/SWI2
1306	49	10.6	2172	2	T20145	hypothetical prote
1307	49	10.6	3164	1	WMBEH6	UL36 protein - hum
1308	48.5	10.5	73	2	D91146	hypothetical prote
1309	48.5	10.5	73	2	H85991	hypothetical prote
1310	48.5	10.5	73	2	E65119	hypothetical 7.5 k
1311	48.5	10.5	75	2	T45361	hypothetical prote
1312	48.5	10.5	115	1	SPRBG	substance P gamma
1313	48.5	10.5	116	2	AD2124	hypothetical prote
1314	48.5	10.5	139	2	G71033	hypothetical prote
1315	48.5	10.5	146	1	A47481	interleukin-13 pre
1316	48.5	10.5	165	2	A31635	neural cell adhesi
1317	48.5	10.5	171	2	JE0153	mitochondrial inne
1318	48.5	10.5	180	2	I40562	hypothetical 20.1K
1319	48.5	10.5	183	2	B81237	hypothetical prote
1320	48.5	10.5	183	2	G82008	probable integral
1321	48.5	10.5	193	2	C97891	hypothetical prote
1322	48.5	10.5	198	2	S75989	endopeptidase Clp
1323	48.5	10.5	199	2	T38524	ATP synthase subun
1324	48.5	10.5	199	2	A69859	hypothetical prote
1325	48.5	10.5	208	2	C89697	protein K02B9.4 [i
1326	48.5	10.5	211	2	C59091	hypothetical prote
1327	48.5	10.5	217	2	A98196	hypothetical prote
1328	48.5	10.5	221	2	D64907	membrane protein y
1329	48.5	10.5	225	2	F81977	hypothetical prote
1330	48.5	10.5	225	2	A86043	probable transposa
1331	48.5	10.5	226	2	T23233	hypothetical prote
1332	48.5	10.5	235	2	AC2809	conserved hypothet
1333	48.5	10.5	235	2	H97587	hypothetical 25.1K
1334	48.5	10.5	241	2	D84138	hypothetical prote
1335	48.5	10.5	243	2	B96010	conserved hypothet
1336	48.5	10.5	245	2	E97425	flagellar biosynth
1337	48.5	10.5	245	2	AE2643	flagellar biosynth
1338	48.5	10.5	256	2	D86544	NADH (ubiquinone)
1339	48.5	10.5	256	2	H72078	probable sodium-tr
1340	48.5	10.5	257	2	AI2741	conserved hypothet
1341	48.5	10.5	257	2	H97522	hypothetical prote
1342	48.5	10.5	257	2	G87509	hypothetical prote
1343	48.5	10.5	258	2	H70487	cytochrome-c oxida
1344	48.5	10.5	269	2	G87134	enoyl-[ACP] reduct
1345	48.5	10.5	273	2	JS0172	chlorophyll a/b-bi
1346	48.5	10.5	276	2	D41044	octopine-binding p
1347	48.5	10.5	277	2	D64666	glutamine ABC tran
1348	48.5	10.5	277	2	G71849	amino acid ABC tra
1349	48.5	10.5	278	2	AB2254	hypothetical prote
1350	48.5	10.5	283	2	B86331	F6F9.15 protein -
1351	48.5	10.5	283	2	D71130	probable oligopept
1352	48.5	10.5	290	2	F71167	hypothetical prote
1353	48.5	10.5	291	2	F81444	probable integral
1354	48.5	10.5	302	2	A75432	3-hydroxybutyryl-C
1355	48.5	10.5	312	2	I40201	mgtE protein - Bac
1356	48.5	10.5	318	2	B91177	probable hemin per
1357	48.5	10.5	330	2	C86023	hypothetical prote
1358	48.5	10.5	332	2	AC0260	hypothetical phage
1359	48.5	10.5	334	2	C81794	hypothetical prote
1360	48.5	10.5	340	2	E83126	ferric enterobacti
1361	48.5	10.5	342	2	E71359	hypothetical prote
1362	48.5	10.5	355	2	T47527	hypothetical prote
1363	48.5	10.5	365	2	F87552	dprA protein [impo
1364	48.5	10.5	370	2	AE0289	conserved hypothet
1365	48.5	10.5	372	2	C39371	Ig V-region-like B
1366	48.5	10.5	382	2	AI0040	probable methanol
1367	48.5	10.5	387	2	H88012	protein K10B4.2 [i
1368	48.5	10.5	388	2	T33908	hypothetical prote
1369	48.5	10.5	394	2	AE1940	two-component resp
1370	48.5	10.5	398	2	F75417	L-sorbosone dehydr
1371	48.5	10.5	400	2	AG1208	cell-division prot
1372	48.5	10.5	400	2	AB1565	cell-division prot
1373	48.5	10.5	401	2	B72329	hypothetical prote
1374	48.5	10.5	406	2	T31778	hypothetical prote
1375	48.5	10.5	409	2	B85735	probable membrane
1376	48.5	10.5	410	2	C86835	hypothetical prote
1377	48.5	10.5	416	2	T02194	probable pectinace
1378	48.5	10.5	421	2	E90883	hypothetical prote
1379	48.5	10.5	424	2	T31978	hypothetical prote
1380	48.5	10.5	425	2	T25873	hypothetical prote
1381	48.5	10.5	426	2	B75434	UDP-N-acetylglucos
1382	48.5	10.5	426	2	T45767	hypothetical prote
1383	48.5	10.5	428	2	JQ1864	hypothetical 47.0K
1384	48.5	10.5	431	2	H70731	probable esterase
1385	48.5	10.5	436	2	I39973	alkaline serine pr
1386	48.5	10.5	441	2	H89809	hypothetical prote
1387	48.5	10.5	443	2	H70430	K+ transport prote
1388	48.5	10.5	461	2	C98120	glycerol-3-phospha
1389	48.5	10.5	463	2	E81141	xanthine/uracil pe
1390	48.5	10.5	467	2	T32292	hypothetical prote
1391	48.5	10.5	470	1	P2WL39	L2 protein - human
1392	48.5	10.5	473	2	T17260	hypothetical prote
1393	48.5	10.5	475	2	T08753	hypothetical prote
1394	48.5	10.5	478	2	D64895	probable membrane
1395	48.5	10.5	500	2	AD1047	probable amino aci
1396	48.5	10.5	509	2	A96563	probable protein k
1397	48.5	10.5	510	2	B72007	conserved hypothet
1398	48.5	10.5	511	2	H90439	hypothetical prote
1399	48.5	10.5	518	2	T05196	hypothetical prote
1400	48.5	10.5	528	2	E81186	L-lactate permease
1401	48.5	10.5	537	2	A75123	proline permease (
1402	48.5	10.5	546	1	VGNZRK	cell fusion glycop
1403	48.5	10.5	546	2	S47305	gene F protein - r
1404	48.5	10.5	553	2	C84920	hypothetical prote
1405	48.5	10.5	553	2	T06499	Rieske [2Fe-2S] ir
1406	48.5	10.5	556	2	S68408	aplysianin A precu
1407	48.5	10.5	559	2	C75286	hypothetical prote
1408	48.5	10.5	578	2	B82204	methyl-accepting c
1409	48.5	10.5	583	2	A70723	probable acyl-coAs
1410	48.5	10.5	584	1	VCMSIA	env polyprotein pr
1411	48.5	10.5	590	2	C86465	probable inositol
1412	48.5	10.5	598	2	A69609	carbon starvation
1413	48.5	10.5	601	2	G96558	probable protein k
1414	48.5	10.5	605	2	T15291	sphingomyelin phos
1415	48.5	10.5	608	2	C95255	hypothetical prote
1416	48.5	10.5	610	2	AI1110	two-component sens

1417	48.5	10.5	611	2	AH3540	ABC transporter AT
1418	48.5	10.5	627	2	D75393	serine proteinase,
1419	48.5	10.5	634	2	AE2558	hypothetical prote
1420	48.5	10.5	638	2	S22490	acetolactate synth
1421	48.5	10.5	639	2	JC4881	polyvinyl-alcohol
1422	48.5	10.5	647	2	T39141	hypothetical prote
1423	48.5	10.5	656	1	ISBYT3	DNA topoisomerase
1424	48.5	10.5	681	2	T39814	hypothetical prote
1425	48.5	10.5	685	2	T32571	hypothetical prote
1426	48.5	10.5	688	2	T13237	NADH2 dehydrogenas
1427	48.5	10.5	693	2	T25878	hypothetical prote
1428	48.5	10.5	693	2	D90441	ABC transporter, p
1429	48.5	10.5	694	2	T13572	NADH2 dehydrogenas
1430	48.5	10.5	694	2	T13573	NADH2 dehydrogenas
1431	48.5	10.5	701	2	T13568	NADH2 dehydrogenas
1432	48.5	10.5	702	2	T12677	NADH2 dehydrogenas
1433	48.5	10.5	702	2	T13505	NADH2 dehydrogenas
1434	48.5	10.5	703	2	T12696	NADH2 dehydrogenas
1435	48.5	10.5	703	2	T13393	NADH2 dehydrogenas
1436	48.5	10.5	704	2	T13665	NADH2 dehydrogenas
1437	48.5	10.5	704	2	T13503	NADH2 dehydrogenas
1438	48.5	10.5	705	2	T04400	NADH2 dehydrogenas
1439	48.5	10.5	706	2	T13391	NADH2 dehydrogenas
1440	48.5	10.5	761	1	IJHUNG	neural cell adhesi
1441	48.5	10.5	763	2	E96571	hypothetical prote
1442	48.5	10.5	764	2	T07608	chloride channel p
1443	48.5	10.5	773	2	T00502	probable receptor-
1444	48.5	10.5	776	2	AB0998	probable transcrip
1445	48.5	10.5	777	2	G90666	probable DNA prima
1446	48.5	10.5	795	2	AD0296	phenylalanine-tRNA
1447	48.5	10.5	796	2	B85517	alpha replication
1448	48.5	10.5	808	2	A82877	hypothetical prote
1449	48.5	10.5	810	2	A64742	hypothetical prote
1450	48.5	10.5	810	2	C90651	hypothetical prote
1451	48.5	10.5	810	2	C85502	hypothetical prote
1452	48.5	10.5	830	1	B48723	replication licens
1453	48.5	10.5	856	2	G96814	hypothetical prote
1454	48.5	10.5	858	2	E96602	hypothetical prote
1455	48.5	10.5	878	2	T17245	hypothetical prote
1456	48.5	10.5	902	2	S49931	SYG1 protein - yea
1457	48.5	10.5	924	2	B41359	potassium channel
1458	48.5	10.5	984	2	C84781	hypothetical prote
1459	48.5	10.5	1011	2	C87789	protein C34G6.6 [i
1460	48.5	10.5	1020	2	AE0701	tetrathionate redu
1461	48.5	10.5	1027	2	I38759	zinc finger/leucin
1462	48.5	10.5	1039	2	T43678	tetratricopeptide
1463	48.5	10.5	1214	2	AG2897	conserved hypothet
1464	48.5	10.5	1262	1	B48758	protein-tyrosine-p
1465	48.5	10.5	1330	2	H89567	protein T08A9.1 [i
1466	48.5	10.5	1363	2	T43220	insulin-like growt
1467	48.5	10.5	1387	2	A97673	probable periplasm
1468	48.5	10.5	1496	1	A48758	protein-tyrosine-p
1469	48.5	10.5	1501	2	I58148	protein-tyrosine-p
1470	48.5	10.5	1747	2	AC1842	WD-40 repeat prote
1471	48.5	10.5	1863	2	S46217	protein-tyrosine-p
1472	48.5	10.5	1902	2	S06997	lactocepin (EC 3.4
1473	48.5	10.5	1902	2	B45764	lactocepin (EC 3.4
1474	48.5	10.5	1907	2	S50893	protein-tyrosine-p
1475	48.5	10.5	1918	2	S43719	lactase (EC 3.2.1.
1476	48.5	10.5	1920	2	S43721	lactase (EC 3.2.1.
1477	48.5	10.5	1926	2	S01169	beta-glycosidase c
1478	48.5	10.5	1962	2	A32634	lactocepin (EC 3.4
1479	48.5	10.5	2175	1	S03170	homeotic protein c
1480	48.5	10.5	2303	1	GNNYTP	genome polyprotein
1481	48.5	10.5	2303	2	S13554	genome polyprotein
1482	48.5	10.5	3187	2	JC5837	364K Golgi complex
1483	48	10.4	99	2	F71031	probable ribosomal
1484	48	10.4	100	2	B69410	hypothetical prote
1485	48	10.4	105	2	E71132	hypothetical prote
1486	48	10.4	109	2	E70730	hypothetical prote
1487	48	10.4	110	2	E69801	hypothetical prote
1488	48	10.4	113	2	AH0397	probable lipoprote
1489	48	10.4	118	2	F87447	hypothetical prote
1490	48	10.4	124	2	AB1977	cytochrome [import
1491	48	10.4	127	2	AI0456	preprotein translo
1492	48	10.4	139	2	D90050	hypothetical prote
1493	48	10.4	148	2	A97062	peptodoglycan-bind
1494	48	10.4	160	2	A71428	hypothetical prote
1495	48	10.4	174	2	S74666	DnaJ protein - Syn
1496	48	10.4	178	2	T19064	hypothetical prote
1497	48	10.4	179	2	S52802	hypothetical prote
1498	48	10.4	182	2	T07641	pEARLI 1 protein h
1499	48	10.4	183	2	T37965	probable 40s ribos
1500	48	10.4	189	2	T34657	probable transcrip

ALIGNMENTS

RESULT 1
I59391
transmembrane protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I59391
R;Attali, B.; Latter, H.; Rachamim, N.; Garty, H.
Proc. Natl. Acad. Sci. U.S.A. 92, 6092-6096, 1995
A;Title: A corticosteroid-induced gene expressing an 'IsK-like' K+ channel activity in
A;Reference number: I59391; MUID:95320221; PMID:7597086
A;Accession: I59391
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-87 <RES>
A;Cross-references: UNIPROT:Q63113; UNIPARC:UPI000012ADF7; GB:L41254; NID:g951422; PIDN:
C;Genetics:
A;Gene: 3D CHIF

Query Match 55.6%; Score 256.5; DB 2; Length 87;
Best Local Similarity 61.5%; Pred. No. 2.8e-21;
Matches 56; Conservative 11; Mismatches 17; Indels 7; Gaps 4;

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Qy          1 MERVTLA-LLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              || :| | ||:|||| ||||  |  :|  ||||||::||| |:| |||| |||||  |||
Db          1 MEGITCAFLLVLAGLPVLEANGP-VDKGSPFYYDWESLQLGGMIFGGLLCIAGIAMALSG 59

Qy         60 KCKYKSSQKQHSP--VPEKAIPLITPGSATT 88
              |||    :: |:|  :|||  |||||||:|
Db         60 KCK---CRRNHTPSSLPEKVTPLITPGSAST 87
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RESULT 2
S61552
mammary tumor protein mat8 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S61552; I48648
R;Morrison, B.W.; Leder, P.
Oncogene 9, 3417-3426, 1994
A;Title: neu and ras initiate murine mammary tumors that share genetic markers generall
A;Reference number: I48271; MUID:95060797; PMID:7970700
A;Accession: S61552
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-88 <MOR>
A;Cross-references: UNIPROT:Q61835; UNIPARC:UPI000002114E; EMBL:X93038; NID:g1085067; P
C;Genetics:
A;Gene: mat8
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-88/Product: mammary tumor protein mat8 #status predicted <MAT>

Query Match 52.4%; Score 241.5; DB 2; Length 88;
Best Local Similarity 57.8%; Pred. No. 1.3e-19;
Matches 52; Conservative 11; Mismatches 24; Indels 3; Gaps 3;

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Qy          1 MERVTLALL-LLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              |: | |:|| |||||  |:||||  ||:|||||||| :|:: |||| |:|   ||  ::||
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Db          1 MQEVVLSLLVLLAGLPTLDANDP-ENKNDPFYYDWYSLRVGGLICAGILCALGIIVLMSG 59

Qy         60 KCKYKSSQKQHSPVPEKAIPLITPGSATTC 89
              ||| |  ||  |  | :  ||||||||  |
Db         60 KCKCKFRQKP-SHRPGEGPPLITPGSAHNC 88


RESULT 3
A55571
chloride conductance inducer Mat-8 - human
C;Species: Homo sapiens (man)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55571
R;Morrison, B.W.; Moorman, J.R.; Kowdley, G.C.; Kobayashi, Y.M.; Jones, L.R.; Leder, P.
J. Biol. Chem. 270, 2176-2182, 1995
A;Title: Mat-8, a novel phospholemman-like protein expressed in human breast tumors, ind
A;Reference number: A55571; MUID:95138184; PMID:7836447
A;Accession: A55571
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-87 <MOR>
A;Cross-references: UNIPROT:Q14802; UNIPARC:UPI0000052765; GB:X93036; GB:S74645; NID:g10
C;Keywords: transmembrane protein

  Query Match             46.5%;  Score 214.5;  DB 2;  Length 87;
  Best Local Similarity   54.5%;  Pred. No. 1.2e-16;
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Qy          1 MERVTLALLL-LAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              |::||| ||: |||   |:|||   :|: |||||| :||: |||| |:|   ||  |:|
Db          1 MQKVTLGLLVFLAGFPVLDAND-LEDKNSPFYYDWHSLQVGGLICAGVLCAMGIIIVMSA 59

Qy         60 KCKYKSSQKQ-HSPVPEKAIPLITPGSA 86
              ||| |  ||  |   | :  ||||||||
Db         60 KCKCKFGQKSGHH--PGETPPLITPGSA 85


RESULT 4
A40533
cAMP-dependent protein kinase major membrane substrate precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 09-Jul-2004
C;Accession: A40533
R;Palmer, C.J.; Scott, B.T.; Jones, L.R.
J. Biol. Chem. 266, 11126-11130, 1991
A;Title: Purification and complete sequence determination of the major plasma membrane s
A;Reference number: A40533; MUID:91250422; PMID:1710217
A;Accession: A40533
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <PAL>
A;Cross-references: UNIPROT:P56513; UNIPARC:UPI0000131C15; GB:M63934

  Query Match             27.4%;  Score 126.5;  DB 2;  Length 92;
  Best Local Similarity   41.4%;  Pred. No. 7.1e-07;
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Qy          8 LLLLAG-LTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKSS 66
              |:|  | ||   |  |   : ||| ||:::|:: |||  |:| | ||  ||| :|: | :
Db          8 LVLCVGFLTTATAEAP--QEHDPFTYDYQSLRIGGLIIAGILFILGILIVLSRRCRCKFN 65

Qy         67 QKQHSPVPEK 76
              |:| :  |::
Db         66 QQQRTGEPDE 75


RESULT 5
D46435
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: D46435; S31525
R;Mercer, R.W.; Biemesderfer, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.
J. Cell Biol. 121, 579-586, 1993
A;Title: Molecular cloning and immunological characterization of the gamma polypeptide,
A;Reference number: A46435; MUID:93252993; PMID:8387529
A;Accession: D46435
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-58 <MER>
A;Cross-references: UNIPROT:Q04645; UNIPARC:UPI00001262A7; EMBL:X70059; NID:g396; PIDN:C
A;Note: the authors translated the codon TTC for residue 25 as Pro
C;Keywords: hydrolase; transmembrane protein

  Query Match             20.9%;  Score 96.5;  DB 2;  Length 58;
  Best Local Similarity   34.6%;  Pred. No. 0.00092;
  Matches   18;  Conservative   14;  Mismatches   19;  Indels    1;  Gaps    1;

Qy         27 DDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKSSQKQHSPVPEKAI 78
              :||||||:: ::  |||   |  | ||:  :|| : :   :::||  :||  :
Db          8 EDPFYYDYETVRNGGLIFAALAFIVGLVIILSKRFRC-GAKRQHRQIPEDGL 58


RESULT 6
A46435
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - sheep (fragment)
N;Alternate names: sodium pump gamma chain; sodium/potassium-dependent ATPase gamma chai
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 22-Nov-1993 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: A46435; S31524; A27383
R;Mercer, R.W.; Biemesderfer, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.
J. Cell Biol. 121, 579-586, 1993
A;Title: Molecular cloning and immunological characterization of the gamma polypeptide,
A;Reference number: A46435; MUID:93252993; PMID:8387529
A;Accession: A46435
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 6-53 <MER>
A;Cross-references: UNIPROT:Q04680; UNIPARC:UPI000017CC97
A;Experimental source: kidney
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:131232, NCBIP:131233)
R;Mercer, R.W.
submitted to the EMBL Data Library, December 1992
A;Description: Cloning and sequencing of gamma subunit of sodium potassium ATPase.
A;Reference number: S31522
A;Accession: S31524
A;Molecule type: mRNA
A;Residues: 6-19,'F',21-53 <MEW>
A;Cross-references: UNIPARC:UPI000016C4B7; EMBL:X70061; NID:g1255; PIDN:CAA49665.1; PID:
R;Collins, J.H.; Leszyk, J.
Biochemistry 26, 8665-8668, 1987
A;Title: The "gamma-subunit" of Na,K-ATPase: a small, amphiphilic protein with a unique
A;Reference number: A27383; MUID:88163544; PMID:2831947
A;Accession: A27383
A;Molecule type: protein
A;Residues: 1-19,'F',21-33 <COL>
A;Cross-references: UNIPARC:UPI000017CC98
C;Complex: heterotrimer; alpha, beta, and gamma chain
C;Keywords: heterotrimer; hydrolase; transmembrane protein

  Query Match             20.5%;  Score 94.5;  DB 2;  Length 53;
  Best Local Similarity   34.6%;  Pred. No. 0.0014;
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Qy         27 DDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKSSQKQHSPVPEKAI 78
              :||||||:: ::  |||   |  | |:  :|| : :   ::|:|  :||  :
Db          3 EDPFYYDYETVRNGGLIPAALAFIVGLVIILSKRFRC-GAKKKHRQIPEDGL 53


RESULT 7
B46435
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: B46435; S31523
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R;Mercer, R.W.; Biemesderfer, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.
J. Cell Biol. 121, 579-586, 1993
A;Title: Molecular cloning and immunological characterization of the gamma polypeptide,
A;Reference number: A46435; MUID:93252993; PMID:8387529
A;Accession: B46435
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-58 <MER>
A;Cross-references: UNIPROT:Q04679; UNIPARC:UPI0000170985; EMBL:X70062; NID:g56299; PIDN
A;Note: the authors translated the codon TTC for residue 25 as Pro
C;Keywords: hydrolase; transmembrane protein

  Query Match             16.4%;  Score 75.5;  DB 2;  Length 58;
  Best Local Similarity   34.7%;  Pred. No. 0.19;
  Matches   17;  Conservative   12;  Mismatches   19;  Indels    1;  Gaps    1;

Qy         27 DDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKSSQKQHSPVPE 75
              ::|| ||:: ::  |||  ||  : |:  :|| : :    | |:|  | |
Db          8 ENPFEYDYETVRKGGLIFAGLAFVVGLLILLSKRFRCGGS-KKHRQVNE 55


RESULT 8
C46435
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: C46435; S31522
R;Mercer, R.W.; Biemesderfer, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.
J. Cell Biol. 121, 579-586, 1993
A;Title: Molecular cloning and immunological characterization of the gamma polypeptide,
A;Reference number: A46435; MUID:93252993; PMID:8387529
A;Accession: C46435
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-58 <MER>
A;Cross-references: UNIPROT:Q04646; UNIPARC:UPI00001482CD; EMBL:X70060; NID:g51111; PIDN
A;Note: the authors translated the codon TTC for residue 25 as Pro
C;Keywords: hydrolase; transmembrane protein

  Query Match             15.9%;  Score 73.5;  DB 2;  Length 58;
  Best Local Similarity   32.7%;  Pred. No. 0.32;
  Matches   16;  Conservative   12;  Mismatches   20;  Indels    1;  Gaps    1;

Qy         27 DDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKSSQKQHSPVPE 75
              ::|| ||:: ::  |||  ||  : |:  :|| : :      |:|  | |
Db          8 ENPFEYDYETVRKGGLIFAGLAFVVGLLIILSKRFRC-GGGKKHRQVNE 55


RESULT 9
A61088
plastoquinol-plastocyanin reductase (EC 1.10.99.1) 17K protein - Synechocystis sp. (stra
N;Alternate names: cytochrome b6-f complex chain IV; plastoquinol-plastocyanin reductase
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A61088; S76298; S15474
R;Osiewacz, H.D.
Arch. Microbiol. 157, 336-342, 1992
A;Title: Construction of insertion mutants of Synechocystis sp. PCC 6803: evidence for a
A;Reference number: A61088; MUID:92272582; PMID:1590707
A;Accession: A61088
A;Molecule type: DNA
A;Residues: 1-160 <OSI>
A;Cross-references: UNIPROT:P27589; UNIPARC:UPI0000131690; EMBL:X58522; NID:g47376; PIDN
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76298
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-160 <KAN>
A;Cross-references: UNIPARC:UPI0000131690; EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: petD
C;Superfamily: cytochrome b6-f complex, subunit 4 (plastoquinol-plastocyanin reductase,
C;Keywords: oxidoreductase; photosynthesis; thylakoid
F;24-144/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>

  Query Match             15.6%;  Score 72;  DB 1;  Length 160;
  Best Local Similarity   37.7%;  Pred. No. 1.4;
  Matches   23;  Conservative    9;  Mismatches   21;  Indels    8;  Gaps    2;

Qy          7 ALLLLAGLTAL------EANDPFANKDD--PFYYDWKNLQLSGLICGGLLAIAGIAAVLS 58
              || |:|||  |       |  ||||   :  | :| :   |:  ::   || |||:||:
Db         47 ALGLIAGLAILDPAMIGEPADPFATPLEILPEWYLYPTFQILRILPNKLLGIAGMAAIPL 106

Qy         59 G 59
              |
Db        107 G 107


RESULT 10
F69989
conserved hypothetical protein ytcJ - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69989
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69989
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-529 <KUN>
A;Cross-references: UNIPROT:O34355; UNIPARC:UPI00000608E4; GB:Z99119; GB:AL009126; NID:
A;Experimental source: strain 168
C;Genetics:
A;Gene: ytcJ

  Query Match             15.4%;  Score 71;  DB 2;  Length 529;
  Best Local Similarity   30.4%;  Pred. No. 6.2;
  Matches   31;  Conservative    9;  Mismatches   24;  Indels   38;  Gaps    6;

Qy         16 ALEANDPFANKDDPFYYD-----------WKNLQLSGLICGG----------LLAIAG 52
              ||:     |   | |:  |            || |   |::| |            || |
Db        381 ALDLQPHFVASDFPWVIDRLGKDRMKTAFAWKTLISKGILCAGGSDAPIEPVDPLLGIQ- 439

Qy         53 IAAVLSGKCKYKSSQKQHSP-------VP-EKAIPLITPGSA 86
                :|||     ||| :|: |       :|  :|| | | |||
Db        440 -SAVLR-----KSSHEQNGPSYNESECLPVYEAIKLYTEGSA 475


RESULT 11
AH0371
probable membrane protein YPO3057 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH0371
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
```

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0371
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-150 <KUR>
A;Cross-references: UNIPROT:Q8ZCD4; UNIPARC:UPI00000CD9C4; GB:AL590842; PIDN:CAC92299.1;
C;Genetics:
A;Gene: YPO3057
C;Superfamily: hypothetical protein ytwI

Query Match 15.0%; Score 69; DB 2; Length 150;
Best Local Similarity 30.2%; Pred. No. 2.7;
Matches 26; Conservative 14; Mismatches 32; Indels 14; Gaps 4;

```
Qy          4 VTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGI-AAVLSGKCK 62
              |||||:|:|  :      |          :: |  ::  ||  | |:   |: | : ||  |
Db         26 VTLAILILIAIRITPLNS---------FFPW--VEKYGLTIGVLILTIGVMAPIASG--K 72

Qy         63 YKSSQKQHSPVPEKAIPLITPGSATT 88
                :|:  || |  |:|  |  | | :
Db         73 ISASEVLHSFVQWKSILAIVVGVAVS 98
```

RESULT 12
A05009
hypothetical protein 135 - liverwort (Marchantia polymorpha) chloroplast
C;Species: chloroplast Marchantia polymorpha
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: S01571; A05009
R;Umesono, K.; Inokuchi, H.; Shiki, Y.; Takeuchi, M.; Chang, Z.; Fukuzawa, H.; Kohchi, T
J. Mol. Biol. 203, 299-331, 1988
A;Title: Structure and organization of Marchantia polymorpha chloroplast genome. II. Gen
A;Reference number: S01567; MUID:89068686; PMID:2974085
A;Accession: S01571
A;Molecule type: DNA
A;Residues: 1-135 <UME>
A;Cross-references: UNIPROT:Q32616; UNIPARC:UPI000013A518; EMBL:X04465; NID:g11640; PIDN
R;Ohyama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi
Nature 322, 572-574, 1986
A;Title: Chloroplast gene organization deduced from complete sequence of liverwort March
A;Reference number: A38014
A;Contents: annotation; gene organization, sites, features
C;Genetics:
A;Genome: chloroplast
A;Introns: 36/1
C;Superfamily: hypothetical protein 135
C;Keywords: chloroplast

Query Match 14.6%; Score 67.5; DB 2; Length 135;
Best Local Similarity 32.6%; Pred. No. 3.6;
Matches 15; Conservative 11; Mismatches 13; Indels 7; Gaps 2;

```
Qy          9 LLLAG--LTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAG 52
              |:: |  | ||:  :|: ::|  |::       ||:|||:|   |
Db         16 LIIIGLFLYALKLREPYVSRDYDFFF-----SCIGLLCGGILFFQG 56
```

RESULT 13
B86620
chorismate synthase [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: B86620
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: B86620
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-359 <STO>
A;Cross-references: UNIPROT:Q9Z6M2; UNIPARC:UPI0000125F94; GB:BA000008; NID:g8979410; PI
A;Experimental source: strain J138
C;Genetics:
A;Gene: aroC
C;Superfamily: chorismate synthase

Query Match 14.4%; Score 66.5; DB 2; Length 359;
Best Local Similarity 23.6%; Pred. No. 13;
Matches 25; Conservative 14; Mismatches 36; Indels 31; Gaps 4;

```
Qy          7 ALLLLAGLTALEANDPFANKD-------DPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              ||: :      |    ||:         |||  : :|: |    ||| |    |   : |
Db        234 ALMSIPAAKGFEIGKGFASAQMRGSQYTDPFVMEGENITLKSNNCGGTLGGITIGVPIEG 293

Qy         60 KCKYK--SSQK--------------------QHSP-VPEKAIPLI 81
              :  :|  || |                    :| | |  :|:|::
Db        294 RIAFKPTSSIKRPCATVTKTKKETTYRTPQTGRHDPCVAIRAVPVV 339
```

RESULT 14
A72004
chorismate synthase CP0815 [imported] - Chlamydophila pneumoniae (strains CWL029 and AR3
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: A72004; D81536
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: A72004
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-359 <ARN>
A;Cross-references: UNIPROT:Q9Z6M2; UNIPARC:UPI0000125F94; GB:AE001684; GB:AE001363; NID
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: D81536
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-359 <REA>
A;Cross-references: UNIPARC:UPI0000125F94; GB:AE002240; GB:AE002161; NID:g7189720; PIDN:
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: aroC; CP0815
C;Superfamily: chorismate synthase

Query Match 14.4%; Score 66.5; DB 2; Length 359;
Best Local Similarity 23.6%; Pred. No. 13;
Matches 25; Conservative 14; Mismatches 36; Indels 31; Gaps 4;

```
Qy          7 ALLLLAGLTALEANDPFANKD-------DPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              ||: :      |    ||:         |||  : :|: |    ||| |    |   : |
Db        234 ALMSIPAAKGFEIGKGFASAQMRGSQYTDPFVMEGENITLKSNNCGGTLGGITIGVPIEG 293

Qy         60 KCKYK--SSQK--------------------QHSP-VPEKAIPLI 81
              :  :|  || |                    :| | |  :|:|::
Db        294 RIAFKPTSSIKRPCATVTKTKKETTYRTPQTGRHDPCVAIRAVPVV 339
```

RESULT 15
A38101
potassium channel KCNA3 - human
N;Alternate names: potassium channel HLK3; potassium channel PCN3; shaker-related potass
C;Species: Homo sapiens (man)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: A38101; B38556; I52990
R;Attali, B.; Romey, G.; Honore, E.; Schmid-Alliana, A.; Mattei, M.G.; Lesage, F.; Ricar

J. Biol. Chem. 267, 8650-8657, 1992
A;Title: Cloning, functional expression, and regulation of two K(+) channels in human T
A;Reference number: A38101; MUID:92235098; PMID:1373731
A;Accession: A38101
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-523 <ATT>
A;Cross-references: UNIPROT:P22001; UNIPARC:UPI000016AB94; GB:M85217; NID:g186664; PIDN:
R;Philipson, L.H.; Hice, R.E.; Schaefer, K.; LaMendola, J.; Bell, G.I.; Nelson, D.J.; St
Proc. Natl. Acad. Sci. U.S.A. 88, 53-57, 1991
A;Title: Sequence and functional expression in Xenopus oocytes of a human insulinoma and
A;Reference number: A38556; MUID:91095456; PMID:1986382
A;Accession: B38556
A;Molecule type: DNA
A;Residues: 1-19,'G',21-36,'V',38-60,'L',62-90,'V',92-337,'S',339-418,'S',420-457,'LS',4
A;Cross-references: UNIPARC:UPI00001779F2; GB:M55515
R;Cai, Y.C.; Osborne, P.B.; North, R.A.; Dooley, D.C.; Douglass, J.
DNA Cell Biol. 11, 163-172, 1992
A;Title: Characterization and functional expression of genomic DNA encoding the human ly
A;Reference number: I52990; MUID:92189730; PMID:1547020
A;Accession: I52990
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-60,'L',62-523 <RES>
A;Cross-references: UNIPARC:UPI0000001C29; GB:M38217; NID:g186670; PIDN:AAB88073.1; PID:
C;Genetics:
A;Gene: GDB:KCNA3; HGK5
A;Cross-references: GDB:128079; OMIM:176263
A;Map position: 1p21-1p13.3
C;Superfamily: potassium channel protein drk1
C;Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; volt

Query Match 14.4%; Score 66.5; DB 2; Length 523;
Best Local Similarity 20.1%; Pred. No. 19;
Matches 30; Conservative 14; Mismatches 36; Indels 69; Gaps 5;

```
Qy          8 LLLLAGLTALEANDP---FANKDDPF-----------YYDWKNLQLSGLICGGLLAIAGI 53
              :|  : :   ||:||   |::  | |           | |   : : | | | | ||||:
Db        358 ILFSSAVYFAEADDPTSGFSSIPDAFWWAVVTMTTVGYGDMHPVTIGGKIVGSLCAIAGV 417

Qy         54 AAVL---------------------------SGKCKYKSSQKQ---------------- 69
                :                           | |:: ||  :
Db        418 LTIALPVPVIVSNFNYFYHRETEGEEQSQYMHVGSCQHLSSSAEELRKARSNSTLSKSEY 477

Qy         70 ---------HSPVPEKAIPLITPGSATTC 89
                     ||  |:   |  |  |  ||
Db        478 MVIEEGGMNHSAFPQ--TPFKTGNSTATC 504
```

Search completed: May 12, 2006, 21:24:50
Job time : 108 secs

GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 12, 2006, 21:18:59 ; Search time 230 Seconds
(without alignments)
273.009 Million cell updates/sec

Title: US-10-063-557-50
Perfect score: 461
Sequence: 1 MERVTLALLLLAGLTALEAN.....HSPVPEKAIPLITPGSATTC 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	461	100.0	89	2	Q6UWZ1_HUMAN	Q6uwz1 homo sapien
2	452	98.0	89	2	Q7Z4M5_HUMAN	Q7z4m5 homo sapien
3	450	97.6	89	1	FXYD4_HUMAN	P59646 homo sapien
4	276.5	60.0	88	1	FXYD4_MOUSE	Q9d2w0 mus musculu
5	256.5	55.6	87	1	FXYD4_RAT	Q63113 rattus norv
6	241.5	52.4	88	1	FXYD3_MOUSE	Q61835 mus musculu
7	234.5	50.9	88	1	FXYD3_RAT	P59645 rattus norv
8	230.5	50.0	88	1	FXYD3_PIG	O97797 sus scrofa
9	214.5	46.5	87	1	FXYD3_HUMAN	Q14802 homo sapien
10	214.5	46.5	87	2	Q6IB59_HUMAN	Q6ib59 homo sapien
11	203	44.0	70	2	Q80UV3_MOUSE	Q80uv3 mus musculu
12	129	28.0	92	1	PLM_HUMAN	O00168 homo sapien
13	127.5	27.7	88	2	Q4RFG2_TETNG	Q4rfg2 tetraodon n
14	126.5	27.4	92	1	PLM_CANFA	P56513 canis famil
15	124.5	27.0	94	1	FXYD6_RAT	Q91xv6 rattus norv
16	123.5	26.8	94	1	FXYD6_MOUSE	Q9d164 mus musculu
17	119	25.8	100	2	Q5M8E9_XENTR	Q5m8e9 xenopus tro
18	116	25.2	94	2	Q70Q12_SQUAC	Q70q12 squalus aca
19	115.5	25.1	92	1	PLM_MOUSE	Q9z239 mus musculu
20	115	24.9	95	1	FXYD6_PONPY	Q5rb29 pongo pygma
21	113.5	24.6	95	2	Q6DJF4_XENLA	Q6djf4 xenopus lae
22	113	24.5	92	1	PLM_RAT	O08589 rattus norv
23	112.5	24.4	95	1	FXYD6_HUMAN	Q9h0q3 homo sapien
24	112.5	24.4	95	1	FXYD6_MACFA	Q4r566 macaca fasc
25	110	23.9	95	2	Q5ZM59_CHICK	Q5zm59 gallus gall
26	107.5	23.3	87	2	Q4RHT7_TETNG	Q4rht7 tetraodon n
27	103.5	22.5	94	2	Q6DJD6_XENLA	Q6djd6 xenopus lae
28	96.5	20.9	58	1	ATNG_BOVIN	Q04645 bos taurus
29	96	20.8	99	2	Q7SZ52_BRARE	Q7sz52 brachydanio
30	95.5	20.7	53	1	ATNG_SHEEP	Q04680 ovis aries
31	95.5	20.7	65	2	Q58K79_PIG	Q58k79 sus scrofa
32	94	20.4	178	1	FXYD5_HUMAN	Q96db9 homo sapien
33	92	20.0	178	1	FXYD5_RAT	P59647 rattus norv
34	92	20.0	178	2	Q6P9W0_RAT	Q6p9w0 rattus norv
35	89	19.3	80	1	FXYD7_HUMAN	P58549 homo sapien
36	85	18.4	80	1	FXYD7_MOUSE	P59648 mus musculu
37	84	18.2	178	2	Q8IWS1_HUMAN	Q8iws1 homo sapien
38	83	18.0	66	1	ATNG_HUMAN	P54710 homo sapien
39	83	18.0	80	1	FXYD7_RAT	P59649 rattus norv
40	83	18.0	94	1	FXYD8_HUMAN	P58550 homo sapien
41	82.5	17.9	66	1	ATNG_RAT	Q04679 rattus norv
42	79.5	17.2	142	2	Q6P8R9_MOUSE	Q6p8r9 mus musculu
43	78	16.9	70	1	ATNG_MOUSE	Q04646 mus musculu
44	78	16.9	70	2	Q6ITT2_MOUSE	Q6itt2 mus musculu
45	77.5	16.8	711	2	Q4NGJ7_9MICC	Q4ngj7 arthrobacte
46	76	16.5	289	2	Q4WU10_ASPFU	Q4wu10 aspergillus
47	75.5	16.4	524	2	Q5LQV1_SILPO	Q5lqv1 silicibacte
48	74	16.1	188	2	Q5LW65_SILPO	Q5lw65 silicibacte
49	74	16.1	208	2	Q4R6E0_MACFA	Q4r6e0 macaca fasc
50	73.5	15.9	64	2	Q6ITT1_MOUSE	Q6itt1 mus musculu
51	73.5	15.9	82	2	Q6ITT0_MOUSE	Q6itt0 mus musculu
52	73.5	15.9	196	2	Q9GZE7_CAEEL	Q9gze7 caenorhabdi
53	73.5	15.9	330	2	Q84EY9_ENTCL	Q84ey9 enterobacte
54	73	15.8	201	2	Q7QJ63_ANOGA	Q7qj63 anopheles g
55	73	15.8	455	2	Q4IPU0_GIBZE	Q4ipu0 gibberella
56	73	15.8	1132	2	Q83861_9REOV	Q83861 nilaparvata
57	73	15.8	1343	2	Q521Q6_MAGGR	Q521q6 magnaporthe
58	72	15.6	160	1	PETD_SYNY3	P27589 synechocyst
59	71	15.4	61	1	ATNG_XENLA	O13001 xenopus lae
60	71	15.4	529	2	O34355_BACSU	O34355 bacillus su
61	70.5	15.3	251	2	Q54FJ8_DICDI	Q54fj8 dictyosteli
62	70.5	15.3	334	2	Q6D644_ERWCT	Q6d644 erwinia car
63	70	15.2	184	1	FXYD5_MOUSE	P97808 mus musculu
64	70	15.2	216	2	Q5ZFS6_PLAMJ	Q5zfs6 plantago ma
65	69.5	15.1	236	2	Q6GME4_XENLA	Q6gme4 xenopus lae
66	69.5	15.1	268	2	Q4FSL8_9GAMM	Q4fsl8 psychrobact
67	69.5	15.1	458	2	Q5KUP7_GEOKA	Q5kup7 geobacillus
68	69	15.0	150	2	Q8ZCD4_YERPE	Q8zcd4 yersinia pe
69	69	15.0	150	2	Q668G1_YERPS	Q668g1 yersinia ps
70	69	15.0	157	2	Q8D0Y1_YERPE	Q8d0y1 yersinia pe
71	68.5	14.9	339	2	Q9LUK8_ARATH	Q9luk8 arabidopsis
72	68.5	14.9	340	2	Q94EI9_ARATH	Q94ei9 arabidopsis
73	68.5	14.9	456	2	Q9CL30_PASMU	Q9cl30 pasteurella
74	68.5	14.9	485	2	Q58EK5_BRARE	Q58ek5 brachydanio
75	68.5	14.9	499	2	Q5VHU4_CIOIN	Q5vhu4 ciona intes
76	68.5	14.9	531	2	Q5VHU5_CIOIN	Q5vhu5 ciona intes
77	68	14.8	173	2	Q8HKR3_9PENC	Q8hkr3 arcos sp. k
78	68	14.8	417	2	Q4QD23_LEIMA	Q4qd23 leishmania
79	68	14.8	978	2	Q69SP5_ORYSA	Q69sp5 oryza sativ
80	67.5	14.6	135	1	YCF66_MARPO	Q32616 marchantia
81	67.5	14.6	337	2	Q6L3V4_SOLDE	Q6l3v4 solanum dem
82	67.5	14.6	387	2	Q6YYY7_ORYSA	Q6yyy7 oryza sativ
83	67.5	14.6	664	2	O75485_HUMAN	O75485 homo sapien
84	67.5	14.6	664	2	Q8WU17_HUMAN	Q8wu17 homo sapien
85	67.5	14.6	664	2	Q5RBT7_PONPY	Q5rbt7 pongo pygma
86	67	14.5	364	2	Q5ZFS7_PLAMJ	Q5zfs7 plantago ma
87	67	14.5	390	1	AROC_SULTO	Q96y94 sulfolobus
88	67	14.5	715	2	Q72E54_DESVH	Q72e54 desulfovibr
89	66.5	14.4	198	2	Q51VA7_MAGGR	Q51va7 magnaporthe
90	66.5	14.4	241	2	Q9K3I3_STRCO	Q9k3i3 streptomyce
91	66.5	14.4	329	2	Q60D39_SOLTU	Q60d39 solanum tub
92	66.5	14.4	359	1	AROC_CHLPN	Q9z6m2 chlamydia p
93	66.5	14.4	516	2	Q28656_RABIT	Q28656 oryctolagus
94	66.5	14.4	523	1	KCNA3_HUMAN	P22001 homo sapien
95	66.5	14.4	546	2	Q5RA50_PONPY	Q5ra50 pongo pygma
96	66.5	14.4	549	2	Q8E9W6_SHEON	Q8e9w6 shewanella
97	66.5	14.4	557	2	Q6P2D3_HUMAN	Q6p2d3 homo sapien
98	66.5	14.4	575	2	Q5VWN2_HUMAN	Q5vwn2 homo sapien
99	66	14.3	139	2	Q5XWN0_SOLTU	Q5xwn0 solanum tub
100	66	14.3	446	2	Q97UY7_SULSO	Q97uy7 sulfolobus
101	65.5	14.2	161	2	Q55N36_CRYNE	Q55n36 cryptococcu
102	65.5	14.2	161	2	Q5KBG5_CRYNE	Q5kbg5 cryptococcu
103	65.5	14.2	305	2	Q74DY6_GEOSL	Q74dy6 geobacter s
104	65.5	14.2	333	2	Q6L3P2_SOLDE	Q6l3p2 solanum dem

105	65.5	14.2	546	2	Q96NJ9_HUMAN	Q96nj9	homo sapien
106	65.5	14.2	546	2	Q86V42_HUMAN	Q86v42	homo sapien
107	65.5	14.2	582	2	Q8N8P9_HUMAN	Q8n8p9	homo sapien
108	65.5	14.2	1185	2	Q8EG58_SHEON	Q8eg58	shewanella
109	65.5	14.2	1278	2	Q4SW90_TETNG	Q4sw90	tetraodon n
110	65	14.1	134	2	Q5RI57_BRARE	Q5ri57	brachydanio
111	65	14.1	327	2	Q9LVG3_ARATH	Q9lvg3	arabidopsis
112	65	14.1	427	2	Q4U9T1_THEAN	Q4u9t1	theileria a
113	65	14.1	469	2	Q9XDX1_MAGMG	Q9xdx1	magnetospir
114	65	14.1	582	2	Q5UQ22_MIMIV	Q5uq22	mimivirus.
115	65	14.1	760	2	Q90638_CHICK	Q90638	gallus gall
116	65	14.1	832	2	Q4SBS0_TETNG	Q4sbs0	tetraodon n
117	64.5	14.0	155	2	Q9R126_MOUSE	Q9r126	mus musculu
118	64.5	14.0	189	2	Q6C1N8_YARLI	Q6c1n8	yarrowia li
119	64.5	14.0	244	2	Q72EX5_DESVH	Q72ex5	desulfovibr
120	64.5	14.0	311	2	Q4HB57_9DEIO	Q4hb57	deinococcus
121	64.5	14.0	312	2	Q71Y12_LISMF	Q71y12	listeria mo
122	64.5	14.0	372	2	Q5WW34_LEGPL	Q5ww34	legionella
123	64.5	14.0	452	2	Q7T165_BRARE	Q7t165	brachydanio
124	64.5	14.0	455	2	Q8TZX5_PYRFU	Q8tzx5	pyrococcus
125	64.5	14.0	465	2	O86080_RHOSH	O86080	rhodobacter
126	64.5	14.0	550	2	Q9QEW7_9PARA	Q9qew7	measles vir
127	64.5	14.0	550	2	Q9QEW9_9PARA	Q9qew9	measles vir
128	64.5	14.0	633	2	Q4SHG0_TETNG	Q4shg0	tetraodon n
129	64.5	14.0	677	2	Q5GUQ5_XANOR	Q5guq5	xanthomonas
130	64.5	14.0	725	2	Q8SY05_DROME	Q8sy05	drosophila
131	64.5	14.0	871	2	Q5A4X3_CANAL	Q5a4x3	candida alb
132	64.5	14.0	920	2	Q6XR97_9BACT	Q6xr97	uncultured
133	64.5	14.0	1750	2	Q4WRY3_ASPFU	Q4wry3	aspergillus
134	64	13.9	186	2	Q4RHT5_TETNG	Q4rht5	tetraodon n
135	64	13.9	250	2	Q7WU64_9THEM	Q7wu64	thermotoga
136	64	13.9	303	2	Q4KGC4_PSEF5	Q4kgc4	pseudomonas
137	64	13.9	315	2	Q9LSS8_ARATH	Q9lss8	arabidopsis
138	64	13.9	340	2	Q72W35_LEPIC	Q72w35	leptospira
139	64	13.9	383	2	Q6N5J0_RHOPA	Q6n5j0	rhodopseudo
140	64	13.9	436	2	Q86VR7_HUMAN	Q86vr7	homo sapien
141	64	13.9	525	1	KCNA3_RAT	P15384	rattus norv
142	64	13.9	582	2	Q6K620_ORYSA	Q6k620	oryza sativ
143	64	13.9	667	2	Q9BJM1_TRISP	Q9bjm1	trichinella
144	64	13.9	678	2	Q8R9G1_THETN	Q8r9g1	thermoanaer
145	64	13.9	727	2	Q6FIK3_CANGA	Q6fik3	candida gla
146	64	13.9	804	2	Q75GV0_ORYSA	Q75gv0	oryza sativ
147	64	13.9	915	2	Q7MG71_VIBVY	Q7mg71	vibrio vuln
148	64	13.9	1046	2	Q82WK5_NITEU	Q82wk5	nitrosomona
149	63.5	13.8	241	2	Q5UX90_HALMA	Q5ux90	haloarcula
150	63.5	13.8	309	2	Q8Y5P7_LISMO	Q8y5p7	listeria mo
151	63.5	13.8	309	2	Q92A05_LISIN	Q92a05	listeria in
152	63.5	13.8	318	2	Q4IG61_GIBZE	Q4ig61	gibberella
153	63.5	13.8	327	2	Q6ZVM5_HUMAN	Q6zvm5	homo sapien
154	63.5	13.8	359	2	Q822F8_CHLCV	Q822f8	chlamydophi
155	63.5	13.8	372	2	Q5X4P4_LEGPA	Q5x4p4	legionella
156	63.5	13.8	396	2	Q5UVL7_9PEZI	Q5uvl7	cercophora
157	63.5	13.8	410	2	Q4LUJ0_9BURK	Q4luj0	burkholderi
158	63.5	13.8	420	2	Q6I568_ORYSA	Q6i568	oryza sativ
159	63.5	13.8	452	2	Q6FVH0_CANGA	Q6fvh0	candida gla
160	63.5	13.8	511	1	KCNC1_HUMAN	P48547	homo sapien
161	63.5	13.8	511	1	KCNC1_MOUSE	P15388	mus musculu
162	63.5	13.8	511	2	Q5BN35_RABIT	Q5bn35	oryctolagus
163	63.5	13.8	511	2	Q5BN36_BOVIN	Q5bn36	bos taurus
164	63.5	13.8	521	2	Q4V7K2_XENLA	Q4v7k2	xenopus lae
165	63.5	13.8	550	2	Q9QEW8_9PARA	Q9qew8	measles vir
166	63.5	13.8	585	1	KCNC1_RAT	P25122	rattus norv
167	63.5	13.8	585	2	Q9XSJ8_CANFA	Q9xsj8	canis famil
168	63.5	13.8	620	2	Q7U2A5_MYCBO	Q7u2a5	mycobacteri
169	63.5	13.8	620	2	O07239_MYCTU	O07239	mycobacteri
170	63.5	13.8	642	2	Q4SZN6_TETNG	Q4szn6	tetraodon n
171	63.5	13.8	725	2	Q4HL36_CAMLA	Q4hl36	campylobact
172	63.5	13.8	747	2	Q575Z7_MAIZE	Q575z7	zea mays (m
173	63	13.7	80	2	Q7NU33_CHRVO	Q7nu33	chromobacte
174	63	13.7	125	2	Q5JJ33_PYRKO	Q5jj33	pyrococcus
175	63	13.7	201	2	Q5N5M0_SYNP6	Q5n5m0	synechococc
176	63	13.7	378	2	Q7QFG1_ANOGA	Q7qfg1	anopheles g
177	63	13.7	465	2	Q4PDK1_USTMA	Q4pdk1	ustilago ma
178	63	13.7	467	2	Q4I5E1_GIBZE	Q4i5e1	gibberella
179	63	13.7	468	2	Q9ZVA7_ARATH	Q9zva7	arabidopsis
180	63	13.7	496	2	Q7NBZ8_MYCGA	Q7nbz8	mycoplasma
181	63	13.7	622	2	Q59QY3_CANAL	Q59qy3	candida alb
182	63	13.7	655	2	Q8KWT9_STRMU	Q8kwt9	streptococc
183	63	13.7	655	2	Q8DUN3_STRMU	Q8dun3	streptococc
184	63	13.7	750	2	Q59R09_CANAL	Q59r09	candida alb
185	63	13.7	808	2	Q6DD69_XENLA	Q6dd69	xenopus lae
186	63	13.7	825	2	Q993G5_9GAMA	Q993g5	callitrichi
187	63	13.7	912	2	Q8D4M3_VIBVU	Q8d4m3	vibrio vuln
188	63	13.7	917	2	Q5E8X2_VIBF1	Q5e8x2	vibrio fisc
189	63	13.7	923	2	Q9N389_CAEEL	Q9n389	caenorhabdi
190	63	13.7	1022	2	Q27779_SCHMA	Q27779	schistosoma
191	63	13.7	1411	2	Q5AS38_EMENI	Q5as38	aspergillus
192	62.5	13.6	146	2	Q81GY1_BACCR	Q81gy1	bacillus ce
193	62.5	13.6	160	2	Q86FE0_SCHJA	Q86fe0	schistosoma
194	62.5	13.6	163	2	Q73CB6_BACC1	Q73cb6	bacillus ce
195	62.5	13.6	207	2	Q8TBL6_HUMAN	Q8tbl6	homo sapien
196	62.5	13.6	286	2	Q9BSB3_HUMAN	Q9bsb3	homo sapien
197	62.5	13.6	299	1	COMQ_BACSU	P33690	bacillus su
198	62.5	13.6	303	2	Q9UNZ3_HUMAN	Q9unz3	homo sapien
199	62.5	13.6	339	2	Q53HE8_HUMAN	Q53he8	homo sapien
200	62.5	13.6	339	2	Q96BY9_HUMAN	Q96by9	homo sapien
201	62.5	13.6	339	2	Q9Y683_HUMAN	Q9y683	homo sapien
202	62.5	13.6	372	2	Q5ZUY1_LEGPH	Q5zuy1	legionella
203	62.5	13.6	434	2	Q6HHZ7_BACHK	Q6hhz7	bacillus th
204	62.5	13.6	434	2	Q81PR7_BACAN	Q81pr7	bacillus an
205	62.5	13.6	492	2	Q750E3_ASHGO	Q750e3	ashbya goss
206	62.5	13.6	504	2	Q7S9U0_NEUCR	Q7s9u0	neurospora
207	62.5	13.6	525	2	O76235_TRYCO	O76235	trypanosoma
208	62.5	13.6	525	2	Q9NCZ9_TRYCO	Q9ncz9	trypanosoma
209	62.5	13.6	539	2	Q9RD59_STRCO	Q9rd59	streptomyce
210	62.5	13.6	557	2	Q7XQW8_ORYSA	Q7xqw8	oryza sativ
211	62.5	13.6	580	2	Q5T6S3_HUMAN	Q5t6s3	homo sapien
212	62.5	13.6	604	2	Q9VNP7_DROME	Q9vnp7	drosophila
213	62.5	13.6	621	2	Q6N038_HUMAN	Q6n038	homo sapien
214	62.5	13.6	663	2	Q72PX8_LEPIC	Q72px8	leptospira
215	62.5	13.6	663	2	Q8F6A7_LEPIN	Q8f6a7	leptospira
216	62.5	13.6	670	2	Q4SQ15_TETNG	Q4sq15	tetraodon n
217	62.5	13.6	685	2	Q8EEJ6_SHEON	Q8eej6	shewanella
218	62.5	13.6	700	2	Q8TG00_ASPFU	Q8tg00	aspergillus
219	62.5	13.6	700	2	Q4WS89_ASPFU	Q4ws89	aspergillus
220	62.5	13.6	760	2	Q7XNU5_ORYSA	Q7xnu5	oryza sativ
221	62.5	13.6	769	1	KCNC3_MOUSE	Q63959	mus musculu
222	62.5	13.6	850	2	Q65MA9_BACLD	Q65ma9	bacillus li
223	62.5	13.6	910	1	SYL_NEIMA	Q9jw39	neisseria m
224	62.5	13.6	1048	1	SILA_SALTY	Q9zhc9	salmonella
225	62.5	13.6	1048	2	Q6MXQ0_SERMA	Q6mxq0	serratia ma
226	62	13.4	150	2	Q893N4_CLOTE	Q893n4	clostridium
227	62	13.4	179	1	DSBB_HAEDU	Q7vky2	haemophilus
228	62	13.4	189	2	Q6X9L3_SULIS	Q6x9l3	sulfolobus
229	62	13.4	269	2	Q6YYW5_ORYSA	Q6yyw5	oryza sativ
230	62	13.4	308	2	Q61BX8_CAEBR	Q61bx8	caenorhabdi
231	62	13.4	308	2	Q8BFU1_MOUSE	Q8bfu1	m mus muscu
232	62	13.4	381	2	Q8UC07_AGRT5	Q8uc07	agrobacteri
233	62	13.4	393	2	Q7CWG7_AGRT5	Q7cwg7	agrobacteri
234	62	13.4	414	2	O32383_STRGR	O32383	streptomyce
235	62	13.4	419	2	Q7XTD2_ORYSA	Q7xtd2	oryza sativ
236	62	13.4	445	2	Q96X94_SULTO	Q96x94	sulfolobus
237	62	13.4	470	2	Q8PHB1_XANAC	Q8phb1	xanthomonas
238	62	13.4	489	2	Q65UC0_MANSM	Q65uc0	mannheimia
239	62	13.4	558	2	Q8N1V9_HUMAN	Q8n1v9	homo sapien
240	62	13.4	577	2	Q9V7C4_DROME	Q9v7c4	drosophila
241	62	13.4	581	1	FUR4_SCHPO	Q10279	schizosacch
242	62	13.4	613	2	Q96PR0_HUMAN	Q96pr0	homo sapien
243	62	13.4	629	2	Q86W09_HUMAN	Q86w09	homo sapien
244	62	13.4	638	2	Q96PR1_HUMAN	Q96pr1	homo sapien
245	62	13.4	641	2	Q4LE77_HUMAN	Q4le77	homo sapien
246	62	13.4	777	2	Q51502_PSEAE	Q51502	pseudomonas
247	62	13.4	862	2	Q6MYC9_ASPFU	Q6myc9	aspergillus
248	62	13.4	862	2	Q4WS99_ASPFU	Q4ws99	aspergillus
249	62	13.4	962	2	Q6BZ68_DEBHA	Q6bz68	debaryomyce
250	62	13.4	1025	2	Q4QGS8_LEIMA	Q4qgs8	leishmania

251	62	13.4	1057	2	Q6FTI2_CANGA	Q6fti2	candida gla
252	62	13.4	2325	2	Q9N3X8_CAEEL	Q9n3x8	caenorhabdi
253	61.5	13.3	134	2	Q6TSM0_9BACI	Q6tsm0	bacillus sp
254	61.5	13.3	178	2	Q83E78_COXBU	Q83e78	coxiella bu
255	61.5	13.3	180	2	Q6I5L4_ORYSA	Q6i5l4	oryza sativ
256	61.5	13.3	206	2	Q5JEL8_PYRKO	Q5jel8	pyrococcus
257	61.5	13.3	210	2	Q636E4_BACCZ	Q636e4	bacillus ce
258	61.5	13.3	213	2	Q8FR74_COREF	Q8fr74	corynebacte
259	61.5	13.3	216	2	Q4NJJ0_9MICC	Q4njj0	arthrobacte
260	61.5	13.3	216	2	Q7V8X4_PROMM	Q7v8x4	prochloroco
261	61.5	13.3	260	2	Q89N10_BRAJA	Q89n10	bradyrhizob
262	61.5	13.3	262	2	Q9NB91_AGRIP	Q9nb91	agrotis ips
263	61.5	13.3	301	2	Q55KX5_CRYNE	Q55kx5	cryptococcu
264	61.5	13.3	301	2	Q5KAK4_CRYNE	Q5kak4	cryptococcu
265	61.5	13.3	303	2	Q5R491_PONPY	Q5r491	pongo pygma
266	61.5	13.3	320	2	Q6LPF1_PHOPR	Q6lpf1	photobacter
267	61.5	13.3	327	2	Q6MJX9_BDEBA	Q6mjx9	bdellovibri
268	61.5	13.3	342	1	ISIA_SYNY3	Q55274	synechocyst
269	61.5	13.3	347	2	Q6R1Z2_MOUSE	Q6r1z2	mus musculu
270	61.5	13.3	381	2	Q88VV9_LACPL	Q88vv9	lactobacill
271	61.5	13.3	382	2	Q4Q9N5_LEIMA	Q4q9n5	leishmania
272	61.5	13.3	399	2	Q89MV3_BRAJA	Q89mv3	bradyrhizob
273	61.5	13.3	427	2	Q5WKB5_BACSK	Q5wkb5	bacillus cl
274	61.5	13.3	433	2	Q9K1T7_CHLPN	Q9k1t7	chlamydia p
275	61.5	13.3	433	2	Q9JS97_CHLPN	Q9js97	chlamydia p
276	61.5	13.3	433	2	Q9Z748_CHLPN	Q9z748	chlamydia p
277	61.5	13.3	434	2	Q736Y4_BACC1	Q736y4	bacillus ce
278	61.5	13.3	437	2	Q8NF56_HUMAN	Q8nf56	homo sapien
279	61.5	13.3	445	2	Q57I33_SALCH	Q57i33	salmonella
280	61.5	13.3	445	2	Q5PKR4_SALPA	Q5pkr4	salmonella
281	61.5	13.3	445	2	Q8Z2L3_SALTI	Q8z2l3	salmonella
282	61.5	13.3	445	2	Q8ZL09_SALTY	Q8zl09	salmonella
283	61.5	13.3	458	2	Q6D860_ERWCT	Q6d860	erwinia car
284	61.5	13.3	461	2	Q4FFN8_9LILI	Q4ffn8	acorus amer
285	61.5	13.3	495	2	Q4SRQ6_TETNG	Q4srq6	tetraodon n
286	61.5	13.3	522	2	Q84DU5_LISIV	Q84du5	listeria iv
287	61.5	13.3	523	2	Q84DU4_LISIV	Q84du4	listeria iv
288	61.5	13.3	524	1	P60_LISIV	Q01837	listeria iv
289	61.5	13.3	545	2	Q9QEW6_9PARA	Q9qew6	measles vir
290	61.5	13.3	549	2	Q9V3U6_DROME	Q9v3u6	drosophila
291	61.5	13.3	566	2	Q73L70_TREDE	Q73l70	treponema d
292	61.5	13.3	592	2	Q9PVD1_XENLA	Q9pvd1	xenopus lae
293	61.5	13.3	668	2	Q8BZU9_MOUSE	Q8bzu9	mus musculu
294	61.5	13.3	668	2	Q7TMV1_MOUSE	Q7tmv1	mus musculu
295	61.5	13.3	701	2	Q4G0I9_HUMAN	Q4g0i9	homo sapien
296	61.5	13.3	746	2	Q51KR6_MAGGR	Q51kr6	magnaporthe
297	61.5	13.3	805	2	Q62L28_BURMA	Q62l28	burkholderi
298	61.5	13.3	831	2	Q60XB5_CAEBR	Q60xb5	caenorhabdi
299	61.5	13.3	855	2	Q63TB1_BURPS	Q63tb1	burkholderi
300	61.5	13.3	977	2	Q96RD9_HUMAN	Q96rd9	homo sapien
301	61.5	13.3	977	2	Q5VYK9_HUMAN	Q5vyk9	homo sapien
302	61.5	13.3	990	2	Q6Q4G3_HUMAN	Q6q4g3	homo sapien
303	61.5	13.3	1145	2	Q8GUE7_9LILI	Q8gue7	cymodocea n
304	61.5	13.3	1322	2	Q5AL53_CANAL	Q5al53	candida alb
305	61.5	13.3	1499	2	Q8YK83_ANASP	Q8yk83	anabaena sp
306	61	13.2	100	2	Q6VE83_PSESY	Q6ve83	pseudomonas
307	61	13.2	139	2	Q87HL7_VIBPA	Q87hl7	vibrio para
308	61	13.2	157	2	Q8DV17_STRMU	Q8dv17	streptococc
309	61	13.2	173	2	Q7Q505_ANOGA	Q7q505	anopheles g
310	61	13.2	173	2	Q6MY22_SERMA	Q6my22	serratia ma
311	61	13.2	180	2	Q811G6_MOUSE	Q811g6	mus musculu
312	61	13.2	187	2	Q5HZU1_XENTR	Q5hzu1	xenopus tro
313	61	13.2	238	2	Q5V6G2_HALMA	Q5v6g2	haloarcula
314	61	13.2	268	2	Q9AB59_CAUCR	Q9ab59	caulobacter
315	61	13.2	272	2	Q8G9V3_ECOLI	Q8g9v3	escherichia
316	61	13.2	302	2	O54880_RAT	O54880	rattus norv
317	61	13.2	320	2	Q34086_COCER	Q34086	coccyzus er
318	61	13.2	326	2	Q762D5_MOUSE	Q762d5	mus musculu
319	61	13.2	338	1	LGT_TREDE	P60974	treponema d
320	61	13.2	355	2	Q95592_COTJA	Q95592	coturnix co
321	61	13.2	380	2	Q7PG49_ANOGA	Q7pg49	anopheles g
322	61	13.2	389	2	Q7T197_CHICK	Q7t197	gallus gall
323	61	13.2	395	2	Q988F9_RHILO	Q988f9	rhizobium l
324	61	13.2	413	2	Q59KD6_CANAL	Q59kd6	candida alb
325	61	13.2	461	2	Q9S5F6_ECOLI	Q9s5f6	escherichia
326	61	13.2	461	2	Q7ACQ0_ECO57	Q7acq0	escherichia
327	61	13.2	463	2	Q9V1R1_PYRAB	Q9v1r1	pyrococcus
328	61	13.2	463	2	O59471_PYRHO	O59471	pyrococcus
329	61	13.2	463	2	O85337_ECOLI	O85337	escherichia
330	61	13.2	463	2	Q7DBF2_ECO57	Q7dbf2	escherichia
331	61	13.2	484	2	Q5GXA1_XANOR	Q5gxa1	xanthomonas
332	61	13.2	488	2	Q5Z1J6_NOCFA	Q5z1j6	nocardia fa
333	61	13.2	502	2	Q5DAP6_SCHJA	Q5dap6	schistosoma
334	61	13.2	520	2	Q9SHZ3_ARATH	Q9shz3	arabidopsis
335	61	13.2	542	2	Q5YVG0_NOCFA	Q5yvg0	nocardia fa
336	61	13.2	568	2	Q61FR3_CAEBR	Q61fr3	caenorhabdi
337	61	13.2	638	2	Q6MLY6_BDEBA	Q6mly6	bdellovibri
338	61	13.2	651	2	Q9DDN7_9TELE	Q9ddn7	apteronotus
339	61	13.2	653	2	Q73TB8_MYCPA	Q73tb8	mycobacteri
340	61	13.2	1305	1	TCGAP_MOUSE	Q80yf9	mus musculu
341	61	13.2	1526	2	Q5K7V4_CRYNE	Q5k7v4	cryptococcu
342	61	13.2	1866	2	Q55IB7_CRYNE	Q55ib7	cryptococcu
343	60.5	13.1	86	2	Q82HN5_STRAW	Q82hn5	streptomyce
344	60.5	13.1	163	2	Q5GYF6_XANOR	Q5gyf6	xanthomonas
345	60.5	13.1	176	2	Q9VJP1_DROME	Q9vjp1	drosophila
346	60.5	13.1	210	1	PYRE_BACAN	Q81wf6	bacillus an
347	60.5	13.1	210	1	PYRE_BACC1	Q732i7	bacillus ce
348	60.5	13.1	210	1	PYRE_BACCR	Q819s7	bacillus ce
349	60.5	13.1	210	1	PYRE_BACHK	Q6het2	bacillus th
350	60.5	13.1	210	2	Q4MJ46_BACCE	Q4mj46	bacillus ce
351	60.5	13.1	227	2	Q8RX00_ARATH	Q8rx00	arabidopsis
352	60.5	13.1	253	2	Q6W741_9NEOP	Q6w741	pediculus h
353	60.5	13.1	289	2	Q7S921_NEUCR	Q7s921	neurospora
354	60.5	13.1	295	2	O22885_ARATH	O22885	arabidopsis
355	60.5	13.1	306	2	Q4NYU8_9DELT	Q4nyu8	anaeromyxob
356	60.5	13.1	312	2	Q9KEQ5_BACHD	Q9keq5	bacillus ha
357	60.5	13.1	319	2	Q4YCE8_PLABE	Q4yce8	plasmodium
358	60.5	13.1	326	2	Q97YW6_SULSO	Q97yw6	sulfolobus
359	60.5	13.1	327	2	Q5XWR0_SOLTU	Q5xwr0	solanum tub
360	60.5	13.1	340	2	Q8LAZ5_ARATH	Q8laz5	arabidopsis
361	60.5	13.1	354	2	Q9M9T5_ARATH	Q9m9t5	arabidopsis
362	60.5	13.1	427	2	Q9A315_CAUCR	Q9a315	caulobacter
363	60.5	13.1	434	2	Q4MG72_BACCE	Q4mg72	bacillus ce
364	60.5	13.1	434	2	Q63AK9_BACCZ	Q63ak9	bacillus ce
365	60.5	13.1	434	2	Q81CL5_BACCR	Q81cl5	bacillus ce
366	60.5	13.1	463	2	Q8D167_YERPE	Q8d167	yersinia pe
367	60.5	13.1	463	2	Q66DX2_YERPS	Q66dx2	yersinia ps
368	60.5	13.1	463	2	Q8ZC25_YERPE	Q8zc25	yersinia pe
369	60.5	13.1	474	2	Q63I87_BURPS	Q63i87	burkholderi
370	60.5	13.1	478	2	Q9NK87_DROME	Q9nk87	drosophila
371	60.5	13.1	484	2	Q6R861_9CAUD	Q6r861	bacteriopha
372	60.5	13.1	484	2	Q4ZBP3_9VIRU	Q4zbp3	bacteriopha
373	60.5	13.1	484	2	Q4ZDK0_9VIRU	Q4zdk0	bacteriopha
374	60.5	13.1	516	2	Q9M174_ARATH	Q9m174	arabidopsis
375	60.5	13.1	547	2	Q4R401_MACFA	Q4r401	macaca fasc
376	60.5	13.1	560	2	Q5P1A5_AZOSE	Q5p1a5	azoarcus sp
377	60.5	13.1	618	2	Q9GGW9_9POAL	Q9ggw9	carex backi
378	60.5	13.1	638	1	KCNC2_RAT	P22462	rattus norv
379	60.5	13.1	658	2	Q7V8R1_PROMM	Q7v8r1	prochloroco
380	60.5	13.1	726	2	Q4HSU4_CAMUP	Q4hsu4	campylobact
381	60.5	13.1	728	1	PURL_CAMJE	Q9pny0	campylobact
382	60.5	13.1	728	1	PURL_CAMJR	Q5huk4	campylobact
383	60.5	13.1	728	2	Q4HIH9_CAMCO	Q4hih9	campylobact
384	60.5	13.1	742	2	Q9Q0S7_9INFA	Q9q0s7	influenza a
385	60.5	13.1	776	2	Q7NT42_CHRVO	Q7nt42	chromobacte
386	60.5	13.1	917	2	Q75V17_STAWA	Q75v17	staphylococ
387	60.5	13.1	1038	2	Q7PPM7_ANOGA	Q7ppm7	anopheles g
388	60.5	13.1	1155	2	Q4IUI7_AZOVI	Q4iui7	azotobacter
389	60.5	13.1	1285	2	Q5ISI2_9REOV	Q5isi2	avian ortho
390	60.5	13.1	1285	2	Q5ISI3_9REOV	Q5isi3	avian ortho
391	60.5	13.1	1285	2	Q5ISI4_9REOV	Q5isi4	avian ortho
392	60.5	13.1	1285	2	Q5ISI5_9REOV	Q5isi5	avian ortho
393	60.5	13.1	1285	2	Q5ISI6_9REOV	Q5isi6	avian ortho
394	60.5	13.1	1285	2	Q5ISI7_9REOV	Q5isi7	avian ortho
395	60.5	13.1	1285	2	Q5ISI8_9REOV	Q5isi8	avian ortho
396	60.5	13.1	1285	2	Q5ISI9_9REOV	Q5isi9	avian ortho

397	60.5	13.1	1285	2	Q8JUV1_9REOV	Q8juv1	avian reovi
398	60.5	13.1	1319	2	Q5AYC8_EMENI	Q5ayc8	aspergillus
399	60.5	13.1	1748	2	Q9HGZ5_ASPOR	Q9hgz5	aspergillus
400	60	13.0	71	1	VITB1_XENLA	P19010	xenopus lae
401	60	13.0	165	2	Q8EPX3_OCEIH	Q8epx3	oceanobacil
402	60	13.0	218	2	Q6LT63_PHOPR	Q6lt63	photobacter
403	60	13.0	249	2	Q8WM93_BRARE	Q8wm93	brachydanio
404	60	13.0	269	2	Q8YXA0_ANASP	Q8yxa0	anabaena sp
405	60	13.0	275	2	Q9VLF8_DROME	Q9vlf8	drosophila
406	60	13.0	288	2	Q88IQ0_PSEPK	Q88iq0	pseudomonas
407	60	13.0	316	2	Q9VVN1_DROME	Q9vvn1	drosophila
408	60	13.0	324	2	Q986J3_RHILO	Q986j3	rhizobium l
409	60	13.0	325	2	Q7XMF8_ORYSA	Q7xmf8	oryza sativ
410	60	13.0	341	1	PAX9_HUMAN	P55771	homo sapien
411	60	13.0	342	1	PAX9_MOUSE	P47242	mus musculu
412	60	13.0	342	2	Q8BS81_MOUSE	Q8bs81	mus musculu
413	60	13.0	352	2	Q5DWS5_KARMI	Q5dws5	karlodinium
414	60	13.0	365	2	Q69135_9GAMA	Q69135	human herpe
415	60	13.0	369	2	Q6D4F3_ERWCT	Q6d4f3	erwinia car
416	60	13.0	378	2	Q8AZK9_9GAMA	Q8azk9	human herpe
417	60	13.0	412	2	Q9I3M4_PSEAE	Q9i3m4	pseudomonas
418	60	13.0	497	1	LMP2_EBV	P13285	epstein-bar
419	60	13.0	497	2	Q777H4_9GAMA	Q777h4	human herpe
420	60	13.0	502	2	Q9BGM9_9MAMM	Q9bgm9	tachyglossu
421	60	13.0	518	2	Q9XE01_STRVG	Q9xe01	streptomyce
422	60	13.0	519	2	Q82LQ9_STRAW	Q82lq9	streptomyce
423	60	13.0	524	2	Q7T198_CHICK	Q7t198	gallus gall
424	60	13.0	525	2	Q83J01_SHIFL	Q83j01	shigella fl
425	60	13.0	538	1	YIEC_ECOLI	P26218	escherichia
426	60	13.0	541	2	Q5KNI3_CRYNE	Q5kni3	cryptococcu
427	60	13.0	565	2	Q8VD01_MOUSE	Q8vd01	mus musculu
428	60	13.0	580	2	Q7T195_CHICK	Q7t195	gallus gall
429	60	13.0	605	2	Q7NHD8_GLOVI	Q7nhd8	gloeobacter
430	60	13.0	611	2	Q8BYF6_MOUSE	Q8byf6	m mus muscu
431	60	13.0	616	2	Q9Y1A2_TRYBB	Q9y1a2	trypanosoma
432	60	13.0	616	2	Q581Z5_9TRYP	Q581z5	trypanosoma
433	60	13.0	756	2	Q55Z68_CRYNE	Q55z68	cryptococcu
434	60	13.0	793	2	Q94BY0_ARATH	Q94by0	arabidopsis
435	60	13.0	819	1	US6NL_MOUSE	Q80xc3	mus musculu
436	60	13.0	876	2	Q4ITT5_AZOVI	Q4itt5	azotobacter
437	60	13.0	1056	2	Q4UVW2_XANCP	Q4uvw2	xanthomonas
438	60	13.0	1056	2	Q8P875_XANCP	Q8p875	xanthomonas
439	60	13.0	1157	2	Q6BHA0_DEBHA	Q6bha0	debaryomyce
440	60	13.0	3187	2	Q4S6R6_TETNG	Q4s6r6	tetraodon n
441	60	13.0	5217	1	HTS1_COCCA	Q01886	cochliobolu
442	59.5	12.9	209	2	Q5KMN0_CRYNE	Q5kmn0	cryptococcu
443	59.5	12.9	214	2	Q7N459_PHOLL	Q7n459	photorhabdu
444	59.5	12.9	216	2	Q9GJG8_SALTR	Q9gjg8	salmo trutt
445	59.5	12.9	216	2	Q9GJG9_SALTR	Q9gjg9	salmo trutt
446	59.5	12.9	216	2	Q9GJH0_SALTR	Q9gjh0	salmo trutt
447	59.5	12.9	217	2	Q9GJH3_SALTR	Q9gjh3	salmo trutt
448	59.5	12.9	217	2	Q9GJH4_SALTR	Q9gjh4	salmo trutt
449	59.5	12.9	217	2	Q9GJH6_SALTR	Q9gjh6	salmo trutt
450	59.5	12.9	217	2	Q9GJH7_SALTR	Q9gjh7	salmo trutt
451	59.5	12.9	223	2	Q6PER5_MOUSE	Q6per5	mus musculu
452	59.5	12.9	228	2	Q4RJQ4_TETNG	Q4rjq4	tetraodon n
453	59.5	12.9	260	2	Q86AQ7_DICDI	Q86aq7	dictyosteli
454	59.5	12.9	267	2	Q9CG47_LACLA	Q9cg47	lactococcus
455	59.5	12.9	298	2	Q9KKR2_VIBCH	Q9kkr2	vibrio chol
456	59.5	12.9	341	2	Q880A3_PSESM	Q880a3	pseudomonas
457	59.5	12.9	342	2	Q9G5Z0_9SAUR	Q9g5z0	pseudocalot
458	59.5	12.9	348	2	Q8XKM0_CLOPE	Q8xkm0	clostridium
459	59.5	12.9	356	2	Q9YMW0_NPVLD	Q9ymw0	lymantria d
460	59.5	12.9	384	2	Q72DS9_DESVH	Q72ds9	desulfovibr
461	59.5	12.9	385	2	Q4SSP1_TETNG	Q4ssp1	tetraodon n
462	59.5	12.9	396	2	Q9U3R3_CAEEL	Q9u3r3	caenorhabdi
463	59.5	12.9	397	2	Q8XSK5_RALSO	Q8xsk5	ralstonia s
464	59.5	12.9	426	2	Q6FJK9_CANGA	Q6fjk9	candida gla
465	59.5	12.9	431	2	Q7XTD3_ORYSA	Q7xtd3	oryza sativ
466	59.5	12.9	526	2	Q7VI06_HELHP	Q7vi06	helicobacte
467	59.5	12.9	527	1	TH11_TRYBB	Q06221	trypanosoma
468	59.5	12.9	527	2	Q26765_9TRYP	Q26765	trypanosoma
469	59.5	12.9	528	1	TH12_TRYBB	Q09037	trypanosoma
470	59.5	12.9	579	2	Q5GTF9_WOLTR	Q5gtf9	wolbachia s
471	59.5	12.9	579	2	Q73I66_WOLPM	Q73i66	wolbachia p
472	59.5	12.9	624	2	Q55X46_CRYNE	Q55x46	cryptococcu
473	59.5	12.9	624	2	Q5KMT6_CRYNE	Q5kmt6	cryptococcu
474	59.5	12.9	636	2	Q4ZR96_PSESY	Q4zr96	pseudomonas
475	59.5	12.9	636	2	Q87ZA8_PSESM	Q87za8	pseudomonas
476	59.5	12.9	677	2	Q98TW3_XENLA	Q98tw3	xenopus lae
477	59.5	12.9	715	2	Q8PSH8_METMA	Q8psh8	methanosarc
478	59.5	12.9	735	2	Q5E3S0_VIBF1	Q5e3s0	vibrio fisc
479	59.5	12.9	778	2	Q4RV23_TETNG	Q4rv23	tetraodon n
480	59.5	12.9	841	2	Q8H105_ARATH	Q8h105	arabidopsis
481	59.5	12.9	841	2	Q8RWY4_ARATH	Q8rwy4	arabidopsis
482	59.5	12.9	847	2	Q9SGW2_ARATH	Q9sgw2	arabidopsis
483	59.5	12.9	894	2	Q8T043_DROME	Q8t043	drosophila
484	59.5	12.9	1037	2	Q9VZ53_DROME	Q9vz53	drosophila
485	59.5	12.9	1048	2	Q4NQ40_9DELT	Q4nq40	anaeromyxob
486	59.5	12.9	1138	2	O12371_9VIRU	O12371	laguna negr
487	59.5	12.9	1800	2	Q8I7P5_DICDI	Q8i7p5	dictyosteli
488	59.5	12.9	1800	2	Q54PV1_DICDI	Q54pv1	dictyosteli
489	59	12.8	119	2	Q9GMZ2_PIG	Q9gmz2	sus scrofa
490	59	12.8	130	2	Q8XBD8_ECO57	Q8xbd8	escherichia
491	59	12.8	149	2	Q88UG2_LACPL	Q88ug2	lactobacill
492	59	12.8	150	2	Q6D7R0_ERWCT	Q6d7r0	erwinia car
493	59	12.8	155	2	Q923L7_MOUSE	Q923l7	mus musculu
494	59	12.8	167	2	Q8W9B3_VOMUR	Q8w9b3	vombatus ur
495	59	12.8	169	2	Q744R5_MYCPA	Q744r5	mycobacteri
496	59	12.8	175	2	O79713_FALPE	O79713	falco pereg
497	59	12.8	177	2	Q92AM4_LISIN	Q92am4	listeria in
498	59	12.8	189	2	Q6X9K8_SULIS	Q6x9k8	sulfolobus
499	59	12.8	189	2	Q6X9L0_SULIS	Q6x910	sulfolobus
500	59	12.8	189	2	Q6X9L1_SULIS	Q6x911	sulfolobus
501	59	12.8	189	2	Q6X9L7_SULIS	Q6x917	sulfolobus
502	59	12.8	189	2	Q6X9M0_SULIS	Q6x9m0	sulfolobus
503	59	12.8	215	1	YCHE_ECOLI	P25743	escherichia
504	59	12.8	215	2	Q8FHX1_ECOL6	Q8fhx1	escherichia
505	59	12.8	215	2	Q83RN1_SHIFL	Q83rn1	shigella fl
506	59	12.8	215	2	Q8XDA5_ECO57	Q8xda5	escherichia
507	59	12.8	284	2	Q594H3_9SPHN	Q594h3	agrobacteri
508	59	12.8	293	1	PUR7_BORBR	Q7wmi1	bordetella
509	59	12.8	293	1	PUR7_BORPA	Q7wb15	bordetella
510	59	12.8	293	1	PUR7_BORPE	Q7vy42	bordetella
511	59	12.8	310	2	Q9A4I0_CAUCR	Q9a410	caulobacter
512	59	12.8	326	2	Q577P4_BRUAB	Q577p4	brucella ab
513	59	12.8	326	2	Q8FWG7_BRUSU	Q8fwg7	brucella su
514	59	12.8	326	2	Q8YBV7_BRUME	Q8ybv7	brucella me
515	59	12.8	345	1	ARGC_BACHK	Q6he28	bacillus th
516	59	12.8	345	2	Q635F0_BACCZ	Q635f0	bacillus ce
517	59	12.8	350	2	Q7MQV1_WOLSU	Q7mqv1	wolinella s
518	59	12.8	356	2	Q7XJY8_ORYSA	Q7xjy8	oryza sativ
519	59	12.8	369	2	Q7QZG4_GIALA	Q7qzg4	giardia lam
520	59	12.8	370	2	Q98F86_RHILO	Q98f86	rhizobium l
521	59	12.8	381	2	Q50WF6_ENTHI	Q50wf6	entamoeba h
522	59	12.8	419	2	Q97VB7_SULSO	Q97vb7	sulfolobus
523	59	12.8	420	2	Q926F0_RHIME	Q926f0	rhizobium m
524	59	12.8	425	2	Q836T8_ENTFA	Q836t8	enterococcu
525	59	12.8	447	2	Q605T5_METCA	Q605t5	methylococc
526	59	12.8	448	2	Q7NZN0_CHRVO	Q7nzn0	chromobacte
527	59	12.8	463	2	Q8JHG2_BRARE	Q8jhg2	brachydanio
528	59	12.8	463	2	Q6PC35_BRARE	Q6pc35	brachydanio
529	59	12.8	479	1	NUON2_RHIME	P56911	rhizobium m
530	59	12.8	526	2	Q6X1D5_9RHAB	Q6x1d5	aravan viru
531	59	12.8	552	2	Q4IBY1_GIBZE	Q4iby1	gibberella
532	59	12.8	557	2	Q5R7Q0_PONPY	Q5r7q0	pongo pygma
533	59	12.8	558	2	Q92C60_LISIN	Q92c60	listeria in
534	59	12.8	575	2	Q9QUU4_9MURI	Q9quu4	rattus sp.
535	59	12.8	579	2	Q6U666_KLEPN	Q6u666	klebsiella
536	59	12.8	598	2	Q4SUR0_TETNG	Q4sur0	tetraodon n
537	59	12.8	611	2	Q8WNQ3_PIG	Q8wnq3	sus scrofa
538	59	12.8	623	2	Q53W46_THET8	Q53w46	thermus the
539	59	12.8	653	2	Q5REB6_PONPY	Q5reb6	pongo pygma
540	59	12.8	654	1	KCNA4_MOUSE	Q61423	mus musculu
541	59	12.8	654	1	KCNA4_MUSPF	Q28527	mustela put
542	59	12.8	654	2	Q8CBF8_MOUSE	Q8cbf8	mus musculu

543	59	12.8	655	1	KCNA4_RAT	P15385	rattus norv
544	59	12.8	660	1	KCNA4_BOVIN	Q05037	bos taurus
545	59	12.8	660	2	Q84MG6_ORYSA	Q84mg6	oryza sativ
546	59	12.8	661	2	Q9GLF1_BOVIN	Q9glf1	bos taurus
547	59	12.8	662	2	Q90W36_COLLI	Q90w36	columba liv
548	59	12.8	662	2	Q9YGX8_CHICK	Q9ygx8	gallus gall
549	59	12.8	663	2	Q61VQ2_CAEBR	Q61vq2	caenorhabdi
550	59	12.8	697	2	Q8JG57_XENLA	Q8jg57	xenopus lae
551	59	12.8	700	2	Q5R4E7_PONPY	Q5r4e7	pongo pygma
552	59	12.8	771	2	Q80X33_MOUSE	Q80x33	mus musculu
553	59	12.8	782	2	Q6LKY8_PHOPR	Q6lky8	photobacter
554	59	12.8	787	2	Q5SMW7_ORYSA	Q5smw7	oryza sativ
555	59	12.8	816	2	Q98SV4_ICTPU	Q98sv4	ictalurus p
556	59	12.8	855	2	Q7NBT0_MYCGA	Q7nbt0	mycoplasma
557	59	12.8	857	1	KCNB1_MOUSE	Q03717	mus musculu
558	59	12.8	857	1	KCNB1_RAT	P15387	rattus norv
559	59	12.8	857	2	Q8K0D1_MOUSE	Q8k0d1	mus musculu
560	59	12.8	858	1	KCNB1_HUMAN	Q14721	homo sapien
561	59	12.8	858	1	KCNB1_PIG	O18868	sus scrofa
562	59	12.8	858	1	KCNB1_RABIT	Q9mz19	oryctolagus
563	59	12.8	898	2	Q91592_XENLA	Q91592	xenopus lae
564	59	12.8	907	1	KCNB2_RAT	Q63099	rattus norv
565	59	12.8	911	1	KCNB2_HUMAN	Q92953	homo sapien
566	59	12.8	911	1	KCNB2_RABIT	Q95111	oryctolagus
567	59	12.8	911	2	Q7Z7D0_HUMAN	Q7z7d0	homo sapien
568	59	12.8	911	2	Q4ZHA6_BOVIN	Q4zha6	bos taurus
569	59	12.8	936	2	Q6GNW5_XENLA	Q6gnw5	xenopus lae
570	59	12.8	971	2	Q5AXB1_EMENI	Q5axb1	aspergillus
571	59	12.8	1078	2	Q4ISZ0_AZOVI	Q4isz0	azotobacter
572	59	12.8	1211	2	Q57WZ8_9TRYP	Q57wz8	trypanosoma
573	59	12.8	1463	2	Q4P3P5_USTMA	Q4p3p5	ustilago ma
574	58.5	12.7	133	2	Q8DA24_VIBVU	Q8da24	vibrio vuln
575	58.5	12.7	153	2	Q7MK55_VIBVY	Q7mk55	vibrio vuln
576	58.5	12.7	169	2	Q6MLM7_BDEBA	Q6mlm7	bdellovibri
577	58.5	12.7	182	2	Q9I6C9_PSEAE	Q9i6c9	pseudomonas
578	58.5	12.7	194	2	Q7QBE9_ANOGA	Q7qbe9	anopheles g
579	58.5	12.7	196	1	CLPP_HELHP	Q7vin7	helicobacte
580	58.5	12.7	200	2	Q4TT87_CAEEL	Q4tt87	caenorhabdi
581	58.5	12.7	200	2	Q852L5_ORYSA	Q852l5	oryza sativ
582	58.5	12.7	217	2	Q96XX6_SULTO	Q96xx6	sulfolobus
583	58.5	12.7	221	2	Q4SQX2_TETNG	Q4sqx2	tetraodon n
584	58.5	12.7	222	2	Q7N7R7_PHOLL	Q7n7r7	photorhabdu
585	58.5	12.7	238	2	Q4SDB4_TETNG	Q4sdb4	tetraodon n
586	58.5	12.7	239	2	Q66IB5_BRARE	Q66ib5	brachydanio
587	58.5	12.7	260	1	NRPN_HUMAN	O60259	homo sapien
588	58.5	12.7	260	2	Q8IW69_HUMAN	Q8iw69	homo sapien
589	58.5	12.7	260	2	Q88YT6_LACPL	Q88yt6	lactobacill
590	58.5	12.7	265	2	Q603A7_METCA	Q603a7	methylococc
591	58.5	12.7	299	2	Q7W0P0_BORPE	Q7w0p0	bordetella
592	58.5	12.7	299	2	Q7W3G6_BORPA	Q7w3g6	bordetella
593	58.5	12.7	299	2	Q7WET6_BORBR	Q7wet6	bordetella
594	58.5	12.7	299	2	Q7NWJ4_CHRVO	Q7nwj4	chromobacte
595	58.5	12.7	303	2	Q5XVK9_ARATH	Q5xvk9	arabidopsis
596	58.5	12.7	321	1	TILS_BORPE	Q7vx92	bordetella
597	58.5	12.7	328	2	Q6LEX6_PLAF7	Q6lex6	plasmodium
598	58.5	12.7	336	2	Q828R5_STRAW	Q828r5	streptomyce
599	58.5	12.7	340	2	Q8R782_THETN	Q8r782	thermoanaer
600	58.5	12.7	344	2	Q4NG06_9MICC	Q4ng06	arthrobacte
601	58.5	12.7	352	2	Q5ECR9_CANFA	Q5ecr9	canis famil
602	58.5	12.7	352	2	Q5KSV8_CANFA	Q5ksv8	canis famil
603	58.5	12.7	359	2	Q5L5F2_CHLAB	Q5l5f2	chlamydophi
604	58.5	12.7	366	2	Q89RR9_BRAJA	Q89rr9	bradyrhizob
605	58.5	12.7	372	2	Q8SGX1_9SAUR	Q8sgx1	pareas macu
606	58.5	12.7	383	1	FAD6E_ARATH	P46313	arabidopsis
607	58.5	12.7	383	2	Q8LFZ8_ARATH	Q8lfz8	arabidopsis
608	58.5	12.7	384	2	Q8UAR7_AGRT5	Q8uar7	agrobacteri
609	58.5	12.7	385	2	Q6ZLL9_ORYSA	Q6zll9	oryza sativ
610	58.5	12.7	389	2	Q7CS44_AGRT5	Q7cs44	agrobacteri
611	58.5	12.7	392	2	Q6C9T8_YARLI	Q6c9t8	yarrowia li
612	58.5	12.7	400	1	EFTU_HERAU	P42477	herpetosiph
613	58.5	12.7	409	2	Q8DBZ6_VIBVU	Q8dbz6	vibrio vuln
614	58.5	12.7	411	2	Q9RU03_DEIRA	Q9ru03	deinococcus
615	58.5	12.7	425	1	YOSB_SCHPO	Q9p712	schizosacch
616	58.5	12.7	426	2	O69513_MYCLE	O69513	mycobacteri
617	58.5	12.7	463	2	Q9CB73_MYCLE	Q9cb73	mycobacteri
618	58.5	12.7	471	2	Q4S1G4_TETNG	Q4s1g4	tetraodon n
619	58.5	12.7	482	2	Q97CF4_THEVO	Q97cf4	thermoplasm
620	58.5	12.7	499	2	Q4NDZ1_9MICC	Q4ndz1	arthrobacte
621	58.5	12.7	509	2	Q58NS5_9TRYP	Q58ns5	trypanosoma
622	58.5	12.7	516	2	Q84DM1_LISSE	Q84dm1	listeria se
623	58.5	12.7	516	2	Q84DU3_LISSE	Q84du3	listeria se
624	58.5	12.7	557	2	Q8VZE2_ARATH	Q8vze2	arabidopsis
625	58.5	12.7	565	2	Q83DB5_COXBU	Q83db5	coxiella bu
626	58.5	12.7	587	2	Q9IA29_ONCMY	Q9ia29	oncorhynchu
627	58.5	12.7	633	2	Q9LMH4_ARATH	Q9lmh4	arabidopsis
628	58.5	12.7	639	2	Q4HWW9_GIBZE	Q4hww9	gibberella
629	58.5	12.7	652	2	Q6VTW8_NPVCD	Q6vtw8	choristoneu
630	58.5	12.7	683	2	Q5CN79_CRYHO	Q5cn79	cryptospori
631	58.5	12.7	716	2	Q58QF6_WHEAT	Q58qf6	triticum ae
632	58.5	12.7	716	2	Q53UC8_WHEAT	Q53uc8	triticum ae
633	58.5	12.7	719	2	Q89ZN6_BACTN	Q89zn6	bacteroides
634	58.5	12.7	726	2	Q8HTN2_9MAGN	Q8htn2	ranzania ja
635	58.5	12.7	876	1	SYL_NEIMB	Q9jxt2	neisseria m
636	58.5	12.7	878	2	Q5FAJ3_NEIG1	Q5faj3	neisseria g
637	58.5	12.7	1048	2	Q6EMD9_ECOLI	Q6emd9	escherichia
638	58.5	12.7	1048	2	Q6U5N9_KLEPN	Q6u5n9	klebsiella
639	58.5	12.7	1095	2	Q9C7H5_ARATH	Q9c7h5	arabidopsis
640	58.5	12.7	1105	2	Q5F3N7_CHICK	Q5f3n7	gallus gall
641	58.5	12.7	1189	2	Q44415_9RHIZ	Q44415	agrobacteri
642	58.5	12.7	1346	2	Q52GR8_MAGGR	Q52gr8	magnaporthe
643	58.5	12.7	1720	2	Q4FXS8_LEIMA	Q4fxs8	leishmania
644	58.5	12.7	1817	2	Q7SZF6_XENLA	Q7szf6	xenopus lae
645	58.5	12.7	2473	2	Q95LC7_9MAMM	Q95lc7	tachyglossu
646	58.5	12.7	2710	2	Q8T3G9_CAEEL	Q8t3g9	caenorhabdi
647	58.5	12.7	2712	2	O01808_CAEEL	O01808	caenorhabdi
648	58.5	12.7	5359	2	Q5VKR4_SACER	Q5vkr4	saccharopol
649	58.5	12.7	6193	2	Q8KSQ0_STRCP	Q8ksq0	streptomyce
650	58	12.6	96	2	Q83E08_COXBU	Q83e08	coxiella bu
651	58	12.6	104	2	Q24949_FASHE	Q24949	fasciola he
652	58	12.6	114	1	YDGD_BACSU	P96702	bacillus su
653	58	12.6	120	2	Q4J5Z8_AZOVI	Q4j5z8	azotobacter
654	58	12.6	175	2	Q5WAS8_BACSK	Q5was8	bacillus cl
655	58	12.6	177	2	Q9EUW4_LISIN	Q9euw4	listeria in
656	58	12.6	185	2	Q5PJ65_SALPA	Q5pj65	salmonella
657	58	12.6	185	2	Q8Z152_SALTI	Q8z152	salmonella
658	58	12.6	185	2	Q8ZK73_SALTY	Q8zk73	salmonella
659	58	12.6	196	2	Q9RYZ1_DEIRA	Q9ryz1	deinococcus
660	58	12.6	215	2	Q57NR2_SALCH	Q57nr2	salmonella
661	58	12.6	215	2	Q5PCY5_SALPA	Q5pcy5	salmonella
662	58	12.6	215	2	Q7CQF4_SALTY	Q7cqf4	salmonella
663	58	12.6	215	2	Q8XF20_SALTI	Q8xf20	salmonella
664	58	12.6	232	2	Q5E0Q0_VIBF1	Q5e0q0	vibrio fisc
665	58	12.6	257	1	DPHB_METJA	Q58670	methanococc
666	58	12.6	263	2	Q9FP64_ORYSA	Q9fp64	oryza sativ
667	58	12.6	277	1	RAFR_PEDPE	P43469	pediococcus
668	58	12.6	314	2	Q6IK08_DROME	Q6ik08	drosophila
669	58	12.6	325	2	Q9ELT9_9VIRU	Q9elt9	rice grassy
670	58	12.6	331	2	Q65F35_BACLD	Q65f35	bacillus li
671	58	12.6	333	2	Q8N7W6_HUMAN	Q8n7w6	homo sapien
672	58	12.6	344	2	Q4V1K5_BACCZ	Q4v1k5	bacillus ce
673	58	12.6	344	2	Q6AXV5_RAT	Q6axv5	rattus norv
674	58	12.6	345	1	ARGC_BACAN	Q81m95	bacillus an
675	58	12.6	349	2	Q7MGC8_VIBVY	Q7mgc8	vibrio vuln
676	58	12.6	354	2	Q95HB3_ANAPL	Q95hb3	anas platyr
677	58	12.6	368	2	Q23311_CAEEL	Q23311	caenorhabdi
678	58	12.6	376	2	Q926X9_LISIN	Q926x9	listeria in
679	58	12.6	383	2	Q81BN5_BACCR	Q81bn5	bacillus ce
680	58	12.6	395	2	Q7PSF3_ANOGA	Q7psf3	anopheles g
681	58	12.6	398	1	SELI_MOUSE	Q80ta1	mus musculu
682	58	12.6	398	2	Q9KPH1_VIBCH	Q9kph1	vibrio chol
683	58	12.6	403	2	Q5F7W0_NEIG1	Q5f7w0	neisseria g
684	58	12.6	409	2	Q4MX56_BACCE	Q4mx56	bacillus ce
685	58	12.6	411	2	Q7YQP7_OCHPR	Q7yqp7	ochotona pr
686	58	12.6	440	2	Q4MSY3_BACCE	Q4msy3	bacillus ce
687	58	12.6	440	2	Q6HKY9_BACHK	Q6hky9	bacillus th
688	58	12.6	440	2	Q81FL1_BACCR	Q81fl1	bacillus ce

689	58	12.6	440	2	Q73AS4_BACC1	Q73as4	bacillus ce
690	58	12.6	440	2	Q63DG6_BACCZ	Q63dg6	bacillus ce
691	58	12.6	440	2	Q81SQ4_BACAN	Q81sq4	bacillus an
692	58	12.6	444	2	Q4SMG6_TETNG	Q4smg6	tetraodon n
693	58	12.6	448	2	Q84DP2_LISMO	Q84dp2	listeria mo
694	58	12.6	457	2	Q4KJP7_PSEF5	Q4kjp7	pseudomonas
695	58	12.6	461	2	Q8ZR07_SALTY	Q8zr07	salmonella
696	58	12.6	462	2	Q9RYH5_DEIRA	Q9ryh5	deinococcus
697	58	12.6	486	2	Q6DBW3_BRARE	Q6dbw3	brachydanio
698	58	12.6	487	2	Q4T7M0_TETNG	Q4t7m0	tetraodon n
699	58	12.6	511	2	Q74CB3_GEOSL	Q74cb3	geobacter s
700	58	12.6	541	2	Q9Y1L1_LOCMI	Q9y1l1	locusta mig
701	58	12.6	549	2	Q8GGR2_STRAZ	Q8ggr2	streptomyce
702	58	12.6	552	2	Q4J3Z2_AZOVI	Q4j3z2	azotobacter
703	58	12.6	553	2	Q942J6_ORYSA	Q942j6	oryza sativ
704	58	12.6	614	2	Q7UVX4_RHOBA	Q7uvx4	rhodopirell
705	58	12.6	629	2	O86146_CAMJE	O86146	campylobact
706	58	12.6	674	2	Q8PHZ1_XANAC	Q8phz1	xanthomonas
707	58	12.6	675	2	Q5H226_XANOR	Q5h226	xanthomonas
708	58	12.6	676	2	Q8XQP3_RALSO	Q8xqp3	ralstonia s
709	58	12.6	681	1	GA2L1_HUMAN	Q99501	homo sapien
710	58	12.6	682	2	Q4HUI4_GIBZE	Q4hui4	gibberella
711	58	12.6	695	2	Q4HLX6_CAMLA	Q4hlx6	campylobact
712	58	12.6	743	2	Q6FJV9_CANGA	Q6fjv9	candida gla
713	58	12.6	758	2	Q9VQW0_DROME	Q9vqw0	drosophila
714	58	12.6	767	2	Q51CV0_ENTHI	Q51cv0	entamoeba h
715	58	12.6	778	2	Q60ZP1_CAEBR	Q60zp1	caenorhabdi
716	58	12.6	876	2	Q91593_XENLA	Q91593	xenopus lae
717	58	12.6	978	2	Q5BDP3_EMENI	Q5bdp3	aspergillus
718	58	12.6	1006	2	Q4NI49_9MICC	Q4ni49	arthrobacte
719	58	12.6	1018	2	Q6ALX0_DESPS	Q6alx0	desulfotale
720	58	12.6	1051	2	Q5B9V4_EMENI	Q5b9v4	aspergillus
721	58	12.6	1056	2	Q7S8Q2_NEUCR	Q7s8q2	neurospora
722	58	12.6	1056	2	Q8PJN1_XANAC	Q8pjn1	xanthomonas
723	58	12.6	1109	2	Q7JR52_DROME	Q7jr52	drosophila
724	58	12.6	1135	2	Q9VTB8_DROME	Q9vtb8	drosophila
725	58	12.6	1149	2	Q7KUE4_DROME	Q7kue4	drosophila
726	58	12.6	1821	2	Q7PQL1_ANOGA	Q7pql1	anopheles g
727	58	12.6	1905	2	Q9XTP6_PLABE	Q9xtp6	plasmodium
728	58	12.6	2576	2	Q8JFV5_BRARE	Q8jfv5	brachydanio
729	58	12.6	4836	2	Q4U2R1_MOUSE	Q4u2r1	mus musculu
730	58	12.6	4836	2	O88473_MOUSE	O88473	mus musculu
731	57.5	12.5	71	1	VITB2_XENLA	P19011	xenopus lae
732	57.5	12.5	84	2	Q8T6F5_DROPS	Q8t6f5	drosophila
733	57.5	12.5	128	2	Q9NG96_MAMBR	Q9ng96	mamestra br
734	57.5	12.5	129	2	Q4K8V9_PSEF5	Q4k8v9	pseudomonas
735	57.5	12.5	139	2	Q8Z6V7_SALTI	Q8z6v7	salmonella
736	57.5	12.5	144	2	Q5YXC3_NOCFA	Q5yxc3	nocardia fa
737	57.5	12.5	144	2	Q9ERF0_RAT	Q9erf0	rattus norv
738	57.5	12.5	146	2	Q5LS51_SILPO	Q5ls51	silicibacte
739	57.5	12.5	153	2	Q8K071_MOUSE	Q8k071	mus musculu
740	57.5	12.5	173	2	Q85CX0_9TELE	Q85cx0	salangichth
741	57.5	12.5	184	2	Q5U4U5_XENLA	Q5u4u5	xenopus lae
742	57.5	12.5	194	2	Q5BIN4_BOVIN	Q5bin4	bos taurus
743	57.5	12.5	224	1	CLPP1_SYNPX	Q7ua36	synechococc
744	57.5	12.5	242	2	Q83T33_SALTI	Q83t33	salmonella
745	57.5	12.5	255	2	Q7XQ06_ORYSA	Q7xq06	oryza sativ
746	57.5	12.5	292	2	Q6FUC0_CANGA	Q6fuc0	candida gla
747	57.5	12.5	307	2	Q46720_ECOLI	Q46720	escherichia
748	57.5	12.5	313	2	Q7NWF7_CHRVO	Q7nwf7	chromobacte
749	57.5	12.5	323	2	Q93H09_STRAW	Q93h09	streptomyce
750	57.5	12.5	324	2	Q9S248_STRCO	Q9s248	streptomyce
751	57.5	12.5	337	2	Q8I7B2_FASHE	Q8i7b2	fasciola he
752	57.5	12.5	342	1	ISIA_SYNP2	P31157	synechococc
753	57.5	12.5	353	2	Q9LRS5_ARATH	Q9lrs5	arabidopsis
754	57.5	12.5	355	2	Q4JFC3_MOUSE	Q4jfc3	mus musculu
755	57.5	12.5	356	2	Q9Y941_AERPE	Q9y941	aeropyrum p
756	57.5	12.5	363	2	Q6D0I3_ERWCT	Q6d0i3	erwinia car
757	57.5	12.5	371	2	Q53GK2_HUMAN	Q53gk2	homo sapien
758	57.5	12.5	371	2	Q9J8C7_9NUCL	Q9j8c7	spodoptera
759	57.5	12.5	374	1	OE56_NPVOP	Q83953	orgyia pseu
760	57.5	12.5	379	1	MCP_CAVPO	P70105	cavia porce
761	57.5	12.5	383	2	Q8A186_BACTN	Q8a186	bacteroides
762	57.5	12.5	388	2	Q54466_STRMY	Q54466	streptomyce
763	57.5	12.5	401	2	Q874Z7_PODAN	Q874z7	podospora a
764	57.5	12.5	402	2	Q7Z7Q2_HUMAN	Q7z7q2	homo sapien
765	57.5	12.5	426	2	O57137_9BETA	O57137	human herpe
766	57.5	12.5	433	2	Q4H838_9DEIO	Q4h838	deinococcus
767	57.5	12.5	441	2	Q60NJ4_CAEBR	Q60nj4	caenorhabdi
768	57.5	12.5	446	2	Q6H7Q3_ORYSA	Q6h7q3	oryza sativ
769	57.5	12.5	448	2	Q6NBL7_RHOPA	Q6nbl7	rhodopseudo
770	57.5	12.5	453	2	Q7ZVN2_BRARE	Q7zvn2	brachydanio
771	57.5	12.5	461	2	Q5PM91_SALPA	Q5pm91	salmonella
772	57.5	12.5	461	2	Q8Z8I5_SALTI	Q8z8i5	salmonella
773	57.5	12.5	461	2	Q9I6E1_PSEAE	Q9i6e1	pseudomonas
774	57.5	12.5	461	2	Q65QV2_MANSM	Q65qv2	mannheimia
775	57.5	12.5	502	2	Q5V1D8_HALMA	Q5v1d8	haloarcula
776	57.5	12.5	507	2	Q5PPF5_RAT	Q5ppf5	rattus norv
777	57.5	12.5	517	2	Q8EV45_MYCPE	Q8ev45	mycoplasma
778	57.5	12.5	523	2	Q9I6Z6_PSEAE	Q9i6z6	pseudomonas
779	57.5	12.5	528	1	KCNA3_MOUSE	P16390	mus musculu
780	57.5	12.5	531	2	Q8ERG1_OCEIH	Q8erg1	oceanobacil
781	57.5	12.5	541	2	Q4SFX1_TETNG	Q4sfx1	tetraodon n
782	57.5	12.5	574	2	Q8XQ27_RALSO	Q8xq27	ralstonia s
783	57.5	12.5	581	2	Q6BK68_DEBHA	Q6bk68	debaryomyce
784	57.5	12.5	594	2	Q98PX5_MYCPU	Q98px5	mycoplasma
785	57.5	12.5	603	2	Q4P4K6_USTMA	Q4p4k6	ustilago ma
786	57.5	12.5	636	2	Q86486_9PARA	Q86486	rinderpest
787	57.5	12.5	656	2	Q8K244_MOUSE	Q8k244	mus musculu
788	57.5	12.5	662	1	HEPA_HHV6Z	P52451	human herpe
789	57.5	12.5	662	2	Q9WT01_9BETA	Q9wt01	human herpe
790	57.5	12.5	668	2	Q4UXH5_XANCP	Q4uxh5	xanthomonas
791	57.5	12.5	668	2	Q8P6N7_XANCP	Q8p6n7	xanthomonas
792	57.5	12.5	670	2	Q9BAQ4_9MAGN	Q9baq4	buxus citri
793	57.5	12.5	671	2	Q5AKV5_CANAL	Q5akv5	candida alb
794	57.5	12.5	692	2	Q9BAR1_9MAGN	Q9bar1	buxus glome
795	57.5	12.5	745	1	PURL_HELHP	Q7vf52	helicobacte
796	57.5	12.5	750	2	Q519G2_ENTHI	Q519g2	entamoeba h
797	57.5	12.5	771	2	Q617U6_CAEBR	Q617u6	caenorhabdi
798	57.5	12.5	772	2	Q75JP4_DICDI	Q75jp4	dictyosteli
799	57.5	12.5	794	2	Q6GP40_XENLA	Q6gp40	xenopus lae
800	57.5	12.5	822	2	Q8IQN2_DROME	Q8iqn2	drosophila
801	57.5	12.5	857	1	OPGH_PSEPK	Q88d04	pseudomonas
802	57.5	12.5	865	2	Q61J98_CAEBR	Q61j98	caenorhabdi
803	57.5	12.5	882	2	Q8MQK2_DROME	Q8mqk2	drosophila
804	57.5	12.5	907	2	Q8VY10_ARATH	Q8vy10	arabidopsis
805	57.5	12.5	1012	2	Q8XUM5_RALSO	Q8xum5	ralstonia s
806	57.5	12.5	1071	2	Q993F2_9GAMA	Q993f2	callitrichi
807	57.5	12.5	1625	2	Q6MVD4_NEUCR	Q6mvd4	neurospora
808	57.5	12.5	1681	2	Q4SVT8_TETNG	Q4svt8	tetraodon n
809	57.5	12.5	1696	2	Q4N0K7_THEPA	Q4n0k7	theileria p
810	57.5	12.5	1751	2	Q57V95_9TRYP	Q57v95	trypanosoma
811	57.5	12.5	1902	1	P2P_LACPA	Q02470	lactobacill
812	57.5	12.5	2235	1	CHD7_HUMAN	Q9p2d1	homo sapien
813	57.5	12.5	2322	2	Q60ZN5_CAEBR	Q60zn5	caenorhabdi
814	57.5	12.5	3300	2	Q4N127_THEPA	Q4n127	theileria p
815	57	12.4	105	2	Q4FTI0_9GAMM	Q4fti0	psychrobact
816	57	12.4	148	2	Q8LGH9_ARATH	Q8lgh9	arabidopsis
817	57	12.4	148	2	Q9ZV24_ARATH	Q9zv24	arabidopsis
818	57	12.4	152	2	Q8E595_STRA3	Q8e595	streptococc
819	57	12.4	158	2	Q6FSW5_CANGA	Q6fsw5	candida gla
820	57	12.4	166	2	Q6IJJ1_DROME	Q6ijj1	drosophila
821	57	12.4	171	2	Q5C0A4_SCHJA	Q5c0a4	schistosoma
822	57	12.4	177	2	Q5LKW5_SILPO	Q5lkw5	silicibacte
823	57	12.4	184	2	Q8LE27_ARATH	Q8le27	arabidopsis
824	57	12.4	184	2	Q4TMQ7_9SPHN	Q4tmq7	erythrobact
825	57	12.4	185	1	ADML_RAT	P43145	rattus norv
826	57	12.4	190	1	PYRE_THETN	P58858	thermoanaer
827	57	12.4	228	2	Q83TM7_LISMO	Q83tm7	listeria mo
828	57	12.4	230	2	Q8EG49_SHEON	Q8eg49	shewanella
829	57	12.4	241	2	Q658A8_ORYSA	Q658a8	oryza sativ
830	57	12.4	254	2	O61095_TRYCR	O61095	trypanosoma
831	57	12.4	258	1	UDP_TREPA	O83990	treponema p
832	57	12.4	268	2	Q70FH9_9CYAN	Q70fh9	uncultured
833	57	12.4	269	2	Q8YQW0_ANASP	Q8yqw0	anabaena sp
834	57	12.4	276	2	Q68ES3_XENLA	Q68es3	xenopus lae

835	57	12.4	283	2	Q4V7U2_XENLA	Q4v7u2	xenopus lae
836	57	12.4	291	2	Q5WX66_LEGPL	Q5wx66	legionella
837	57	12.4	292	2	Q6UY47_HUMAN	Q6uy47	homo sapien
838	57	12.4	301	2	Q8BYJ2_MOUSE	Q8byj2	mus musculu
839	57	12.4	302	2	Q768S4_MOUSE	Q768s4	mus musculu
840	57	12.4	315	2	Q9UNE2_HUMAN	Q9une2	homo sapien
841	57	12.4	325	2	Q9QN99_9VIRU	Q9qn99	rice grassy
842	57	12.4	332	2	Q52W67_PAVLU	Q52w67	pavlova lut
843	57	12.4	334	2	Q52W83_BANAT	Q52w83	bangia atro
844	57	12.4	342	1	ISIA_SYNP7	P15347	synechococc
845	57	12.4	342	2	Q5N675_SYNP6	Q5n675	synechococc
846	57	12.4	343	2	Q5LM56_SILPO	Q5lm56	silicibacte
847	57	12.4	351	2	O97774_FELCA	O97774	felis silve
848	57	12.4	352	2	Q867D6_FELCA	Q867d6	felis silve
849	57	12.4	353	2	Q9LR37_ARATH	Q9lr37	arabidopsis
850	57	12.4	355	2	Q5QNA9_ORYSA	Q5qna9	oryza sativ
851	57	12.4	360	2	Q8WBK3_9AVES	Q8wbk3	saurothera
852	57	12.4	374	2	O80638_ARATH	O80638	arabidopsis
853	57	12.4	374	2	Q9SVF3_ARATH	Q9svf3	arabidopsis
854	57	12.4	374	2	Q67ZB8_ARATH	Q67zb8	arabidopsis
855	57	12.4	374	2	Q5NXV2_AZOSE	Q5nxv2	azoarcus sp
856	57	12.4	376	2	Q6FV38_CANGA	Q6fv38	candida gla
857	57	12.4	383	2	Q6HGU3_BACHK	Q6hgu3	bacillus th
858	57	12.4	383	2	Q81NM9_BACAN	Q81nm9	bacillus an
859	57	12.4	384	2	Q65XI0_ORYSA	Q65xi0	oryza sativ
860	57	12.4	385	2	Q9SZG0_ARATH	Q9szg0	arabidopsis
861	57	12.4	386	2	Q5NFP0_FRATT	Q5nfp0	francisella
862	57	12.4	387	2	Q5B694_EMENI	Q5b694	aspergillus
863	57	12.4	387	2	Q6AQC8_DESPS	Q6aqc8	desulfotale
864	57	12.4	399	2	Q53J03_SHIFL	Q53j03	shigella fl
865	57	12.4	409	2	Q639H1_BACCZ	Q639h1	bacillus ce
866	57	12.4	425	2	Q4TR85_9SPHN	Q4tr85	erythrobact
867	57	12.4	440	2	Q9LMU8_ARATH	Q9lmu8	arabidopsis
868	57	12.4	440	2	Q8BJG0_MOUSE	Q8bjg0	mus musculu
869	57	12.4	456	2	Q97N14_CLOAB	Q97n14	clostridium
870	57	12.4	457	1	PROY_ECOLI	P77327	escherichia
871	57	12.4	457	2	Q83SG9_SHIFL	Q83sg9	shigella fl
872	57	12.4	461	1	DCUC_ECOLI	Q47134	escherichia
873	57	12.4	461	2	Q57RU8_SALCH	Q57ru8	salmonella
874	57	12.4	461	2	Q8FJZ8_ECOL6	Q8fjz8	escherichia
875	57	12.4	461	2	Q63M54_BURPS	Q63m54	burkholderi
876	57	12.4	468	2	Q7QD04_ANOGA	Q7qd04	anopheles g
877	57	12.4	471	2	Q5JNB5_ORYSA	Q5jnb5	oryza sativ
878	57	12.4	477	2	Q84DP6_LISMO	Q84dp6	listeria mo
879	57	12.4	477	2	Q84DP7_LISMO	Q84dp7	listeria mo
880	57	12.4	477	2	Q84DP8_LISMO	Q84dp8	listeria mo
881	57	12.4	477	2	Q84DP9_LISMO	Q84dp9	listeria mo
882	57	12.4	477	2	Q84DQ0_LISMO	Q84dq0	listeria mo
883	57	12.4	477	2	Q83TQ3_LISMO	Q83tq3	listeria mo
884	57	12.4	477	2	Q722W8_LISMF	Q722w8	listeria mo
885	57	12.4	478	2	Q84DN9_LISMO	Q84dn9	listeria mo
886	57	12.4	478	2	Q84DS7_LISMO	Q84ds7	listeria mo
887	57	12.4	487	1	PSBC_PORPU	P51356	porphyra pu
888	57	12.4	487	2	Q8H1D7_ARATH	Q8h1d7	arabidopsis
889	57	12.4	487	2	Q93ZU2_ARATH	Q93zu2	arabidopsis
890	57	12.4	493	2	Q7NC13_MYCGA	Q7nc13	mycoplasma
891	57	12.4	494	1	ILVC_PHOPR	Q6lvz5	photobacter
892	57	12.4	517	2	Q88GW6_PSEPK	Q88gw6	pseudomonas
893	57	12.4	531	2	Q60VX5_CAEBR	Q60vx5	caenorhabdi
894	57	12.4	534	2	Q4WGI0_ASPFU	Q4wgi0	aspergillus
895	57	12.4	535	2	Q4KIR3_PSEF5	Q4kir3	pseudomonas
896	57	12.4	576	2	Q8BYE8_MOUSE	Q8bye8	mus musculu
897	57	12.4	606	2	Q88AM8_PSESM	Q88am8	pseudomonas
898	57	12.4	610	2	Q7Z2H9_HUMAN	Q7z2h9	homo sapien
899	57	12.4	610	2	Q8N695_HUMAN	Q8n695	homo sapien
900	57	12.4	629	2	Q4I3Y7_GIBZE	Q4i3y7	gibberella
901	57	12.4	633	2	Q746H7_THET2	Q746h7	thermus the
902	57	12.4	641	2	Q8MJD4_RABIT	Q8mjd4	oryctolagus
903	57	12.4	689	2	Q6A4I8_BUTFI	Q6a4i8	butyrivibri
904	57	12.4	699	2	Q7NII1_GLOVI	Q7nii1	gloeobacter
905	57	12.4	705	2	Q4T7V1_TETNG	Q4t7v1	tetraodon n
906	57	12.4	792	2	Q4RXC8_TETNG	Q4rxc8	tetraodon n
907	57	12.4	802	2	Q7UMP8_RHOBA	Q7ump8	rhodopirell
908	57	12.4	811	2	Q4FXZ2_LEIMA	Q4fxz2	leishmania
909	57	12.4	858	2	Q6ZPE7_MOUSE	Q6zpe7	mus musculu
910	57	12.4	880	2	Q6KI07_MYCMO	Q6ki07	mycoplasma
911	57	12.4	892	2	Q5LUM8_SILPO	Q5lum8	silicibacte
912	57	12.4	953	1	FNBP3_MOUSE	Q9r1c7	mus musculu
913	57	12.4	1056	2	Q5GZ12_XANOR	Q5gz12	xanthomonas
914	57	12.4	1137	2	Q82EI0_STRAW	Q82ei0	streptomyce
915	57	12.4	1151	2	Q754S3_ASHGO	Q754s3	ashbya goss
916	57	12.4	1294	2	Q50HM7_STRSH	Q50hm7	streptomyce
917	57	12.4	1491	2	Q5GF21_HAEIN	Q5gf21	haemophilus
918	57	12.4	1574	2	Q7Y5J5_9CAUD	Q7y5j5	xanthomonas
919	57	12.4	1639	2	Q54J43_DICDI	Q54j43	dictyosteli
920	57	12.4	1875	2	Q5X8U3_LEGPA	Q5x8u3	legionella
921	57	12.4	2660	2	Q7QL19_ANOGA	Q7ql19	anopheles g
922	57	12.4	3196	2	Q6ALQ5_DESPS	Q6alq5	desulfotale
923	57	12.4	3338	2	Q82PH6_STRAW	Q82ph6	streptomyce
924	56.5	12.3	104	2	Q6J2H4_PSEYM	Q6j2h4	pseudomonas
925	56.5	12.3	107	2	Q67MA1_SYMTH	Q67ma1	symbiobacte
926	56.5	12.3	110	2	Q6J932_9LILI	Q6j932	xerophyta h
927	56.5	12.3	114	1	HXD3_RAT	P18867	rattus norv
928	56.5	12.3	120	2	Q6JIA6_HUMAN	Q6jia6	homo sapien
929	56.5	12.3	120	2	Q4MPP5_BACCE	Q4mpp5	bacillus ce
930	56.5	12.3	120	2	Q6HMB7_BACHK	Q6hmb7	bacillus th
931	56.5	12.3	120	2	Q63EV5_BACCZ	Q63ev5	bacillus ce
932	56.5	12.3	120	2	Q81U42_BACAN	Q81u42	bacillus an
933	56.5	12.3	143	2	Q8PLW5_XANAC	Q8plw5	xanthomonas
934	56.5	12.3	145	2	Q75LT0_HUMAN	Q751t0	homo sapien
935	56.5	12.3	145	2	Q869G4_LYMST	Q869g4	lymnaea sta
936	56.5	12.3	148	2	Q9D2U7_MOUSE	Q9d2u7	mus musculu
937	56.5	12.3	148	2	Q99LS0_MOUSE	Q991s0	mus musculu
938	56.5	12.3	170	2	Q9W2N2_DROME	Q9w2n2	drosophila
939	56.5	12.3	186	2	Q6N191_RHOPA	Q6n191	rhodopseudo
940	56.5	12.3	187	2	Q52296_SHIFL	Q52296	shigella fl
941	56.5	12.3	187	2	Q7BEL2_SHIFL	Q7bel2	shigella fl
942	56.5	12.3	188	2	Q5FRN2_GLUOX	Q5frn2	gluconobact
943	56.5	12.3	190	2	Q9JKW1_RAT	Q9jkw1	rattus norv
944	56.5	12.3	191	2	Q57JF1_SALCH	Q57jf1	salmonella
945	56.5	12.3	191	2	Q5PLD9_SALPA	Q5pld9	salmonella
946	56.5	12.3	191	2	Q7CPP0_SALTY	Q7cpp0	salmonella
947	56.5	12.3	191	2	Q8XGY6_SALTI	Q8xgy6	salmonella
948	56.5	12.3	194	1	TIM22_MOUSE	Q9cq85	mus musculu
949	56.5	12.3	194	2	Q5SSL1_MOUSE	Q5ssl1	mus musculu
950	56.5	12.3	194	2	Q9JKW2_MOUSE	Q9jkw2	mus musculu
951	56.5	12.3	195	2	Q8IN78_DROME	Q8in78	drosophila
952	56.5	12.3	197	2	Q8U0L2_PYRFU	Q8u012	pyrococcus
953	56.5	12.3	197	2	Q73KT6_TREDE	Q73kt6	treponema d
954	56.5	12.3	211	2	Q6E5T5_FUGRU	Q6e5t5	fugu rubrip
955	56.5	12.3	213	2	Q8NS64_CORGL	Q8ns64	corynebacte
956	56.5	12.3	214	2	Q4V6C7_DROME	Q4v6c7	drosophila
957	56.5	12.3	228	2	Q84WK4_ARATH	Q84wk4	arabidopsis
958	56.5	12.3	231	2	Q7ULW2_RHOBA	Q7ulw2	rhodopirell
959	56.5	12.3	233	1	LPPX_MYCBO	P65307	mycobacteri
960	56.5	12.3	233	1	LPPX_MYCTU	P65306	mycobacteri
961	56.5	12.3	234	2	Q92LX9_RHIME	Q92lx9	rhizobium m
962	56.5	12.3	244	2	Q8K2G6_MOUSE	Q8k2g6	mus musculu
963	56.5	12.3	258	2	Q9HP14_HALSA	Q9hp14	halobacteri
964	56.5	12.3	274	2	Q4SET1_TETNG	Q4set1	tetraodon n
965	56.5	12.3	276	2	Q937L7_9CYAN	Q93717	uncultured
966	56.5	12.3	276	2	Q937L8_9CYAN	Q93718	uncultured
967	56.5	12.3	288	2	Q826Y5_STRAW	Q826y5	streptomyce
968	56.5	12.3	299	2	Q4SGT7_TETNG	Q4sgt7	tetraodon n
969	56.5	12.3	304	2	Q4H8A0_9DEIO	Q4h8a0	deinococcus
970	56.5	12.3	305	2	Q5ZIU9_CHICK	Q5ziu9	gallus gall
971	56.5	12.3	335	2	Q8G6M8_BIFLO	Q8g6m8	bifidobacte
972	56.5	12.3	337	1	TH23_TRYBB	Q09039	trypanosoma
973	56.5	12.3	337	2	Q9GKE5_RABIT	Q9gke5	oryctolagus
974	56.5	12.3	350	2	Q7UXC7_RHOBA	Q7uxc7	rhodopirell
975	56.5	12.3	354	2	Q60DT9_ORYSA	Q60dt9	oryza sativ
976	56.5	12.3	358	2	Q4UKP7_RICFE	Q4ukp7	rickettsia
977	56.5	12.3	364	2	Q4P2I9_USTMA	Q4p2i9	ustilago ma
978	56.5	12.3	368	2	Q5YVA8_NOCFA	Q5yva8	nocardia fa
979	56.5	12.3	372	2	Q5QNB2_ORYSA	Q5qnb2	oryza sativ
980	56.5	12.3	374	2	Q5I7H1_NPVAP	Q5i7h1	antheraea p

981	56.5	12.3	387	2	Q88LL0_PSEPK	Q88ll0	pseudomonas
982	56.5	12.3	391	2	Q6MLC9_BDEBA	Q6mlc9	bdellovibri
983	56.5	12.3	393	2	Q81JG4_BACAN	Q81jg4	bacillus an
984	56.5	12.3	394	2	Q7QAA4_ANOGA	Q7qaa4	anopheles g
985	56.5	12.3	398	2	Q8LRB6_ORYSA	Q8lrb6	oryza sativ
986	56.5	12.3	403	2	Q7W0P4_BORPE	Q7w0p4	bordetella
987	56.5	12.3	403	2	Q7W3G0_BORPA	Q7w3g0	bordetella
988	56.5	12.3	403	2	Q7WET0_BORBR	Q7wet0	bordetella
989	56.5	12.3	407	2	Q4J3Y8_AZOVI	Q4j3y8	azotobacter
990	56.5	12.3	408	2	Q8EIS5_SHEON	Q8eis5	shewanella
991	56.5	12.3	409	2	Q6LMI6_PHOPR	Q6lmi6	photobacter
992	56.5	12.3	411	2	Q7P149_CHRVO	Q7p149	chromobacte
993	56.5	12.3	414	2	Q4SS40_TETNG	Q4ss40	tetraodon n
994	56.5	12.3	418	2	Q96JU9_HUMAN	Q96ju9	homo sapien
995	56.5	12.3	419	1	CARP_CRYPA	P11838	cryphonectr
996	56.5	12.3	422	2	Q5PBS0_ANAMM	Q5pbs0	anaplasma m
997	56.5	12.3	428	2	Q59H29_HUMAN	Q59h29	homo sapien
998	56.5	12.3	442	2	Q5QXI7_IDILO	Q5qxi7	idiomarina
999	56.5	12.3	464	1	NORM_SYNP6	Q5mzd9	synechococc
1000	56.5	12.3	468	2	Q63PW6_BURPS	Q63pw6	burkholderi
1001	56.5	12.3	468	2	Q62G62_BURMA	Q62g62	burkholderi
1002	56.5	12.3	471	2	O49635_ARATH	O49635	arabidopsis
1003	56.5	12.3	474	2	Q55WA9_CRYNE	Q55wa9	cryptococcu
1004	56.5	12.3	484	2	Q8SDN4_9CAUD	Q8sdn4	staphylococ
1005	56.5	12.3	484	2	Q4ZCK1_9VIRU	Q4zck1	bacteriopha
1006	56.5	12.3	484	2	Q6GGS4_STAAR	Q6ggs4	staphylococ
1007	56.5	12.3	484	2	Q5HIX6_STAAC	Q5hix6	staphylococ
1008	56.5	12.3	485	2	Q7CZR7_AGRT5	Q7czr7	agrobacteri
1009	56.5	12.3	485	2	Q90YY3_XENLA	Q90yy3	xenopus lae
1010	56.5	12.3	491	2	Q4PCU5_USTMA	Q4pcu5	ustilago ma
1011	56.5	12.3	494	2	Q86S12_9DIPT	Q86s12	drosophila
1012	56.5	12.3	500	2	Q97KA2_CLOAB	Q97ka2	clostridium
1013	56.5	12.3	510	2	Q9RF10_MYXXA	Q9rf10	myxococcus
1014	56.5	12.3	511	1	ZGPAT_MOUSE	Q8vdm1	mus musculu
1015	56.5	12.3	521	2	Q7RYH0_NEUCR	Q7ryh0	neurospora
1016	56.5	12.3	523	2	Q567M8_BRARE	Q567m8	brachydanio
1017	56.5	12.3	529	1	TH2A_TRYBB	Q06222	trypanosoma
1018	56.5	12.3	551	2	Q4JXL7_CORJK	Q4jxl7	corynebacte
1019	56.5	12.3	567	2	Q4KI08_PSEF5	Q4ki08	pseudomonas
1020	56.5	12.3	570	2	Q4WD85_ASPFU	Q4wd85	aspergillus
1021	56.5	12.3	577	2	Q85QS0_9INSE	Q85qs0	tricholepid
1022	56.5	12.3	595	1	S13A1_HUMAN	Q9bzw2	homo sapien
1023	56.5	12.3	608	2	Q9BAR2_9MAGN	Q9bar2	notobuxus n
1024	56.5	12.3	614	2	O31615_BACSU	O31615	bacillus su
1025	56.5	12.3	624	2	Q69Z90_MOUSE	Q69z90	mus musculu
1026	56.5	12.3	648	2	Q5FUH5_GLUOX	Q5fuh5	gluconobact
1027	56.5	12.3	670	2	O32212_BACSU	O32212	bacillus su
1028	56.5	12.3	681	2	Q9BAQ3_9MAGN	Q9baq3	notobuxus a
1029	56.5	12.3	683	2	Q5CV27_CRYPV	Q5cv27	cryptospori
1030	56.5	12.3	683	2	Q9BAS3_9MAGN	Q9bas3	buxus micro
1031	56.5	12.3	686	1	VGLH_PRVKA	P27416	pseudorabie
1032	56.5	12.3	686	1	VGLH_PRVN3	Q00660	pseudorabie
1033	56.5	12.3	686	1	VGLH_PRVRI	P27593	pseudorabie
1034	56.5	12.3	686	2	Q5PPA2_9ALPH	Q5ppa2	suid herpes
1035	56.5	12.3	688	2	Q9BAS8_9MAGN	Q9bas8	buxus henry
1036	56.5	12.3	689	2	Q7Q3N1_ANOGA	Q7q3n1	anopheles g
1037	56.5	12.3	690	2	Q9BAS2_9MAGN	Q9bas2	buxus hilde
1038	56.5	12.3	690	2	Q9BAS4_9MAGN	Q9bas4	buxus ripar
1039	56.5	12.3	691	2	Q9BAQ8_BUXSE	Q9baq8	buxus sempe
1040	56.5	12.3	692	2	Q9BAQ9_9MAGN	Q9baq9	buxus liuki
1041	56.5	12.3	692	2	Q9BAR0_9MAGN	Q9bar0	buxus gonoc
1042	56.5	12.3	692	2	Q9BAR5_9MAGN	Q9bar5	buxus balea
1043	56.5	12.3	692	2	Q9BAS5_9MAGN	Q9bas5	buxus micro
1044	56.5	12.3	695	2	Q9BAS7_9MAGN	Q9bas7	buxus harla
1045	56.5	12.3	699	2	Q96SW4_HUMAN	Q96sw4	homo sapien
1046	56.5	12.3	704	2	Q9SCI4_BUXSE	Q9sci4	buxus sempe
1047	56.5	12.3	707	2	Q9BAS6_9MAGN	Q9bas6	buxus macow
1048	56.5	12.3	710	2	Q6C6N0_YARLI	Q6c6n0	yarrowia li
1049	56.5	12.3	726	2	Q8HTM7_PODPE	Q8htm7	podophyllum
1050	56.5	12.3	726	2	Q8HTM9_9MAGN	Q8htm9	sinopodophy
1051	56.5	12.3	729	2	Q5PXK6_RAT	Q5pxk6	rattus norv
1052	56.5	12.3	730	2	Q5PXK5_RAT	Q5pxk5	rattus norv
1053	56.5	12.3	757	1	KCNC3_HUMAN	Q14003	homo sapien
1054	56.5	12.3	758	2	Q811T2_RAT	Q811t2	rattus norv
1055	56.5	12.3	759	2	Q8HXV1_RABIT	Q8hxv1	oryctolagus
1056	56.5	12.3	769	2	Q811T3_RAT	Q811t3	rattus norv
1057	56.5	12.3	783	2	Q5NXT1_AZOSE	Q5nxt1	azoarcus sp
1058	56.5	12.3	852	1	YKM1_YEAST	P32330	saccharomyc
1059	56.5	12.3	856	2	Q6G429_BARHE	Q6g429	bartonella
1060	56.5	12.3	889	1	KCNC3_RAT	Q01956	rattus norv
1061	56.5	12.3	894	2	Q5CGN7_CRYHO	Q5cgn7	cryptospori
1062	56.5	12.3	933	2	Q83GL1_TROWT	Q83gl1	tropheryma
1063	56.5	12.3	939	2	Q83HL6_TROW8	Q83hl6	tropheryma
1064	56.5	12.3	1000	2	Q5U635_HUMAN	Q5u635	homo sapien
1065	56.5	12.3	1009	2	Q5QZ08_IDILO	Q5qz08	idiomarina
1066	56.5	12.3	1030	1	SEM6A_HUMAN	Q9h2e6	homo sapien
1067	56.5	12.3	1058	2	Q5P5T6_AZOSE	Q5p5t6	azoarcus sp
1068	56.5	12.3	1127	2	Q4YY05_PLABE	Q4yy05	plasmodium
1069	56.5	12.3	1241	2	Q60RT2_CAEBR	Q60rt2	caenorhabdi
1070	56.5	12.3	1250	2	Q4P1V2_USTMA	Q4p1v2	ustilago ma
1071	56.5	12.3	1643	2	Q5ZCR4_ORYSA	Q5zcr4	oryza sativ
1072	56.5	12.3	1739	2	Q4SXM5_TETNG	Q4sxm5	tetraodon n
1073	56.5	12.3	1778	2	Q4I4N8_GIBZE	Q4i4n8	gibberella
1074	56.5	12.3	1838	2	Q6BCJ9_TETTH	Q6bcj9	tetrahymena
1075	56.5	12.3	1844	2	Q5BDW2_EMENI	Q5bdw2	aspergillus
1076	56.5	12.3	2113	2	Q4RMA1_TETNG	Q4rma1	tetraodon n
1077	56.5	12.3	2217	2	Q6FNY7_CANGA	Q6fny7	candida gla
1078	56.5	12.3	2876	2	Q4QB73_LEIMA	Q4qb73	leishmania
1079	56.5	12.3	4464	2	Q7RL36_PLAYO	Q7rl36	plasmodium
1080	56	12.1	75	2	Q8E590_STRA3	Q8e590	streptococc
1081	56	12.1	79	1	IVBKI_DENPO	P00981	dendroaspis
1082	56	12.1	100	2	Q6N984_RHOPA	Q6n984	rhodopseudo
1083	56	12.1	103	1	NIRC_PARDE	Q51702	paracoccus
1084	56	12.1	103	2	Q8K2N1_MOUSE	Q8k2n1	mus musculu
1085	56	12.1	126	2	Q573I6_9BACT	Q573i6	uncultured
1086	56	12.1	126	2	Q6J5N4_ECOLI	Q6j5n4	escherichia
1087	56	12.1	146	2	Q4NYQ0_9DELT	Q4nyq0	anaeromyxob
1088	56	12.1	160	2	Q61TQ7_CAEBR	Q61tq7	caenorhabdi
1089	56	12.1	177	2	O62579_GIALA	O62579	giardia lam
1090	56	12.1	177	2	Q7R002_GIALA	Q7r002	giardia lam
1091	56	12.1	196	1	Y286_MYCGE	P47528	mycoplasma
1092	56	12.1	197	2	Q5FUH6_GLUOX	Q5fuh6	gluconobact
1093	56	12.1	212	2	Q87MV9_VIBPA	Q87mv9	vibrio para
1094	56	12.1	218	2	Q9D692_MOUSE	Q9d692	mus musculu
1095	56	12.1	220	2	Q5LEE4_BACFN	Q5lee4	bacteroides
1096	56	12.1	222	2	Q9KVF5_VIBCH	Q9kvf5	vibrio chol
1097	56	12.1	228	2	Q5J432_SALCH	Q5j432	salmonella
1098	56	12.1	230	2	Q5QLP9_ORYSA	Q5qlp9	oryza sativ
1099	56	12.1	242	2	Q6MEA9_PARUW	Q6mea9	parachlamyd
1100	56	12.1	249	2	Q5VTN6_BRARE	Q5vtn6	brachydanio
1101	56	12.1	254	2	Q91207_ONCMY	Q91207	oncorhynchu
1102	56	12.1	261	2	Q8UAP2_AGRT5	Q8uap2	agrobacteri
1103	56	12.1	264	2	Q9CPG1_PASMU	Q9cpg1	pasteurella
1104	56	12.1	274	2	Q4NIS8_9MICC	Q4nis8	arthrobacte
1105	56	12.1	279	1	Y170_BUCBP	Q89as2	buchnera ap
1106	56	12.1	281	2	Q7NU04_CHRVO	Q7nu04	chromobacte
1107	56	12.1	282	2	Q5FIQ7_LACAC	Q5fiq7	lactobacill
1108	56	12.1	283	2	Q525Q1_MAGGR	Q525q1	magnaporthe
1109	56	12.1	286	2	Q9CMZ4_PASMU	Q9cmz4	pasteurella
1110	56	12.1	292	2	Q9U8W8_TACTR	Q9u8w8	tachypleus
1111	56	12.1	294	2	Q6FFJ6_ACIAD	Q6ffj6	acinetobact
1112	56	12.1	295	2	Q7NFB8_GLOVI	Q7nfb8	gloeobacter
1113	56	12.1	302	2	Q7Q9G8_ANOGA	Q7q9g8	anopheles g
1114	56	12.1	304	2	Q8ESB3_OCEIH	Q8esb3	oceanobacil
1115	56	12.1	306	2	Q87HY7_VIBPA	Q87hy7	vibrio para
1116	56	12.1	319	2	Q611Y3_CAEBR	Q611y3	caenorhabdi
1117	56	12.1	319	2	Q505K1_MOUSE	Q505k1	mus musculu
1118	56	12.1	324	2	Q9F487_FISMU	Q9f487	fischerella
1119	56	12.1	325	2	O36172_9VIRU	O36172	rice grassy
1120	56	12.1	334	2	Q52W82_9RHOD	Q52w82	compsopogon
1121	56	12.1	340	2	Q504U7_HUMAN	Q504u7	homo sapien
1122	56	12.1	340	2	Q8F9S3_LEPIN	Q8f9s3	leptospira
1123	56	12.1	342	2	Q5B7Z1_EMENI	Q5b7z1	aspergillus
1124	56	12.1	344	2	Q5AWH7_EMENI	Q5awh7	aspergillus
1125	56	12.1	351	2	Q98EM8_RHILO	Q98em8	rhizobium l
1126	56	12.1	352	2	Q6YT41_PIG	Q6yt41	sus scrofa

1127	56	12.1	354	2	Q6F593_ANAPL	Q6f593	anas platyr
1128	56	12.1	359	2	Q5Z1Y1_NOCFA	Q5z1y1	nocardia fa
1129	56	12.1	361	2	O62896_ICTPU	O62896	ictalurus p
1130	56	12.1	363	2	Q88NF7_PSEPK	Q88nf7	pseudomonas
1131	56	12.1	364	2	Q5UZ44_HALMA	Q5uz44	haloarcula
1132	56	12.1	365	2	Q98IE3_RHILO	Q98ie3	rhizobium l
1133	56	12.1	376	2	Q6CNY1_KLULA	Q6cny1	kluyveromyc
1134	56	12.1	388	2	Q9STX2_ARATH	Q9stx2	arabidopsis
1135	56	12.1	388	2	Q673W2_MOUSE	Q673w2	mus musculu
1136	56	12.1	398	2	Q7XKE3_ORYSA	Q7xke3	oryza sativ
1137	56	12.1	405	2	Q7NYU3_CHRVO	Q7nyu3	chromobacte
1138	56	12.1	408	2	Q7PW26_ANOGA	Q7pw26	anopheles g
1139	56	12.1	409	2	Q87LW6_VIBPA	Q87lw6	vibrio para
1140	56	12.1	411	2	Q9A4V3_CAUCR	Q9a4v3	caulobacter
1141	56	12.1	413	2	Q67T35_SYMTH	Q67t35	symbiobacte
1142	56	12.1	434	1	ENO_DESVM	O32513	desulfovibr
1143	56	12.1	436	1	ALBD1_BACSU	P71008	bacillus su
1144	56	12.1	436	1	ALBD2_BACSU	Q8rkh4	bacillus su
1145	56	12.1	438	2	Q9KYG4_STRCO	Q9kyg4	streptomyce
1146	56	12.1	439	2	Q6BRK2_DEBHA	Q6brk2	debaryomyce
1147	56	12.1	440	2	Q8UIZ8_AGRT5	Q8uiz8	agrobacteri
1148	56	12.1	442	2	Q642S2_XENLA	Q642s2	xenopus lae
1149	56	12.1	445	2	Q4HBN0_9DEIO	Q4hbn0	deinococcus
1150	56	12.1	449	2	O06407_MYCTU	O06407	mycobacteri
1151	56	12.1	449	2	Q7U1T6_MYCBO	Q7u1t6	mycobacteri
1152	56	12.1	450	2	Q6A6T5_PROAC	Q6a6t5	propionibac
1153	56	12.1	452	2	Q6D0K7_ERWCT	Q6d0k7	erwinia car
1154	56	12.1	456	2	Q84DM6_LISMO	Q84dm6	listeria mo
1155	56	12.1	456	2	Q84DM8_LISMO	Q84dm8	listeria mo
1156	56	12.1	456	2	Q84DM9_LISMO	Q84dm9	listeria mo
1157	56	12.1	457	1	DCR1B_CHICK	Q5qjc3	gallus gall
1158	56	12.1	457	2	Q84DM7_LISMO	Q84dm7	listeria mo
1159	56	12.1	457	2	Q84DP4_LISMO	Q84dp4	listeria mo
1160	56	12.1	458	2	Q84DN5_LISMO	Q84dn5	listeria mo
1161	56	12.1	458	2	Q84DN6_LISMO	Q84dn6	listeria mo
1162	56	12.1	459	2	Q5FWL2_XENLA	Q5fwl2	xenopus lae
1163	56	12.1	461	2	Q84DQ5_LISMO	Q84dq5	listeria mo
1164	56	12.1	461	2	Q62D13_BURMA	Q62d13	burkholderi
1165	56	12.1	471	2	Q84DQ3_LISMO	Q84dq3	listeria mo
1166	56	12.1	477	2	Q84DM5_LISMO	Q84dm5	listeria mo
1167	56	12.1	477	2	Q84DN0_LISMO	Q84dn0	listeria mo
1168	56	12.1	477	2	Q84DN1_LISMO	Q84dn1	listeria mo
1169	56	12.1	477	2	Q84DN3_LISMO	Q84dn3	listeria mo
1170	56	12.1	478	2	Q84DP0_LISMO	Q84dp0	listeria mo
1171	56	12.1	479	2	Q84DP3_LISMO	Q84dp3	listeria mo
1172	56	12.1	480	2	Q522N7_MAGGR	Q522n7	magnaporthe
1173	56	12.1	488	2	Q4NEK3_9MICC	Q4nek3	arthrobacte
1174	56	12.1	490	2	Q7N3C6_PHOLL	Q7n3c6	photorhabdu
1175	56	12.1	494	2	Q5V4M5_HALMA	Q5v4m5	haloarcula
1176	56	12.1	503	1	VL1_HPV32	P36737	human papil
1177	56	12.1	503	2	Q5N550_SYNP6	Q5n550	synechococc
1178	56	12.1	508	2	Q8FP11_COREF	Q8fp11	corynebacte
1179	56	12.1	516	2	Q8CE47_MOUSE	Q8ce47	mus musculu
1180	56	12.1	516	2	Q94WJ7_CTEFR	Q94wj7	ctenogobiop
1181	56	12.1	518	2	Q4IHP5_GIBZE	Q4ihp5	gibberella
1182	56	12.1	519	2	Q9VXK1_DROME	Q9vxk1	drosophila
1183	56	12.1	524	2	Q81FE6_BACCR	Q81fe6	bacillus ce
1184	56	12.1	525	2	Q4RW80_TETNG	Q4rw80	tetraodon n
1185	56	12.1	528	2	Q4KCT5_PSEF5	Q4kct5	pseudomonas
1186	56	12.1	531	2	Q4I973_GIBZE	Q4i973	gibberella
1187	56	12.1	539	1	CH60_ENTAG	O66200	enterobacte
1188	56	12.1	539	1	CH60_ENTAS	O66190	enterobacte
1189	56	12.1	540	1	CH60_KLEOR	O66214	klebsiella
1190	56	12.1	540	1	CH60_KLEOX	O66210	klebsiella
1191	56	12.1	544	1	CH60_AERSA	O68309	aeromonas s
1192	56	12.1	545	2	Q6TLJ7_9PSED	Q6tlj7	pseudomonas
1193	56	12.1	547	1	CH60_KLEPN	O66026	klebsiella
1194	56	12.1	547	2	Q92Z88_RHIME	Q92z88	rhizobium m
1195	56	12.1	548	2	Q6Y3X3_XENNE	Q6y3x3	xenorhabdus
1196	56	12.1	557	1	FMO4_HUMAN	P31512	homo sapien
1197	56	12.1	557	2	Q5RDN6_PONPY	Q5rdn6	pongo pygma
1198	56	12.1	558	2	Q53XR0_HUMAN	Q53xr0	homo sapien
1199	56	12.1	559	2	Q6UN75_TOBAC	Q6un75	nicotiana t
1200	56	12.1	568	2	Q4FXC6_LEIMA	Q4fxc6	leishmania
1201	56	12.1	575	2	Q7N243_PHOLL	Q7n243	photorhabdu
1202	56	12.1	576	2	Q7N7S6_PHOLL	Q7n7s6	photorhabdu
1203	56	12.1	578	1	PTF3E_RHOCA	P23387	r pts syste
1204	56	12.1	581	2	Q8C3F7_MOUSE	Q8c3f7	mus musculu
1205	56	12.1	594	2	Q9X3S5_PSEAE	Q9x3s5	pseudomonas
1206	56	12.1	605	2	Q6INM3_XENLA	Q6inm3	xenopus lae
1207	56	12.1	610	2	O76486_LEIME	O76486	leishmania
1208	56	12.1	621	2	Q4PHM9_USTMA	Q4phm9	ustilago ma
1209	56	12.1	621	2	Q660P2_BORGA	Q660p2	borrelia ga
1210	56	12.1	626	2	O51574_BORBU	O51574	borrelia bu
1211	56	12.1	629	2	Q4SJG4_TETNG	Q4sjg4	tetraodon n
1212	56	12.1	632	2	Q93MA1_CLOPE	Q93ma1	clostridium
1213	56	12.1	638	2	Q8C4I5_MOUSE	Q8c4i5	mus musculu
1214	56	12.1	643	2	Q5QN53_ORYSA	Q5qn53	oryza sativ
1215	56	12.1	653	1	KCNA4_HUMAN	P22459	homo sapien
1216	56	12.1	690	2	Q73T97_MYCPA	Q73t97	mycobacteri
1217	56	12.1	712	2	Q54QS3_DICDI	Q54qs3	dictyosteli
1218	56	12.1	724	2	Q8A8Y9_BACTN	Q8a8y9	bacteroides
1219	56	12.1	736	2	O28661_ARCFU	O28661	archaeoglob
1220	56	12.1	752	2	Q4NY34_9DELT	Q4ny34	anaeromyxob
1221	56	12.1	848	2	Q5EE54_9HIV1	Q5ee54	human immun
1222	56	12.1	855	2	Q8A6V6_BACTN	Q8a6v6	bacteroides
1223	56	12.1	917	2	Q4WEX4_ASPFU	Q4wex4	aspergillus
1224	56	12.1	965	2	Q50LF0_9CORY	Q50lf0	corynebacte
1225	56	12.1	1012	2	Q7RCG7_PLAYO	Q7rcg7	plasmodium
1226	56	12.1	1051	2	Q5ZD75_ORYSA	Q5zd75	oryza sativ
1227	56	12.1	1084	2	Q5WVH5_LEGPL	Q5wvh5	legionella
1228	56	12.1	1118	2	Q68M96_RHIME	Q68m96	rhizobium m
1229	56	12.1	1118	2	Q92Y97_RHIME	Q92y97	rhizobium m
1230	56	12.1	1126	2	Q4PEF6_USTMA	Q4pef6	ustilago ma
1231	56	12.1	1135	2	Q5X437_LEGPA	Q5x437	legionella
1232	56	12.1	1243	2	Q4FRM6_9GAMM	Q4frm6	psychrobact
1233	56	12.1	1305	1	FTSK_YERPE	Q8zgc7	yersinia pe
1234	56	12.1	1310	2	Q66CK2_YERPS	Q66ck2	yersinia ps
1235	56	12.1	1384	1	CNTP1_HUMAN	P78357	homo sapien
1236	56	12.1	1406	2	Q6L3G4_SOLDE	Q6l3g4	solanum dem
1237	56	12.1	1439	2	Q7XQP1_ORYSA	Q7xqp1	oryza sativ
1238	56	12.1	1462	2	Q8IIW9_PLAF7	Q8iiw9	plasmodium
1239	56	12.1	1520	2	Q55UE6_CRYNE	Q55ue6	cryptococcu
1240	56	12.1	1608	2	Q59GL0_HUMAN	Q59gl0	homo sapien
1241	56	12.1	1856	1	GBF1_CRIGR	Q9r1d7	cricetulus
1242	56	12.1	1859	1	GBF1_HUMAN	Q92538	homo sapien
1243	56	12.1	1875	2	Q6RCQ2_LEGPN	Q6rcq2	legionella
1244	56	12.1	1875	2	Q5ZZ76_LEGPH	Q5zz76	legionella
1245	56	12.1	1914	1	RLF_HUMAN	Q13129	homo sapien
1246	56	12.1	1914	2	Q5RCL4_PONPY	Q5rcl4	pongo pygma
1247	56	12.1	2055	1	MPDZ_MOUSE	Q8vbx6	mus musculu
1248	56	12.1	3972	2	Q7PMJ6_ANOGA	Q7pmj6	anopheles g
1249	56	12.1	6994	2	Q17343_CAEEL	Q17343	caenorhabdi
1250	56	12.1	6994	2	Q17490_CAEEL	Q17490	caenorhabdi
1251	55.5	12.0	62	2	Q8CKT3_YERPE	Q8ckt3	yersinia pe
1252	55.5	12.0	63	2	Q4FLU9_9RICK	Q4flu9	candidatus
1253	55.5	12.0	84	2	Q5WGD8_BACSK	Q5wgd8	bacillus cl
1254	55.5	12.0	124	2	Q88L31_PSEPK	Q88l31	pseudomonas
1255	55.5	12.0	134	2	Q6TSR7_BACCE	Q6tsr7	bacillus ce
1256	55.5	12.0	138	2	Q5TLI8_MOUSE	Q5tli8	mus musculu
1257	55.5	12.0	141	2	Q6YXR7_PHYPA	Q6yxr7	physcomitre
1258	55.5	12.0	147	2	Q63K49_BURPS	Q63k49	burkholderi
1259	55.5	12.0	147	2	Q62B21_BURMA	Q62b21	burkholderi
1260	55.5	12.0	151	2	Q8DCH7_VIBVU	Q8dch7	vibrio vuln
1261	55.5	12.0	157	2	Q93Z87_BROIN	Q93z87	bromus iner
1262	55.5	12.0	168	2	Q6U398_LACPL	Q6u398	lactobacill
1263	55.5	12.0	177	2	Q4LXV9_9BURK	Q4lxv9	burkholderi
1264	55.5	12.0	179	2	Q6LME1_PHOPR	Q6lme1	photobacter
1265	55.5	12.0	184	2	Q7BKF5_PRB01	Q7bkf5	gamma-prote
1266	55.5	12.0	186	2	Q83JM5_SHIFL	Q83jm5	shigella fl
1267	55.5	12.0	186	2	Q5M7K0_XENTR	Q5m7k0	xenopus tro
1268	55.5	12.0	187	2	Q707B6_ECOLI	Q707b6	escherichia
1269	55.5	12.0	187	2	Q8CVQ9_ECOL6	Q8cvq9	escherichia
1270	55.5	12.0	191	2	Q6E5S2_FUGRU	Q6e5s2	fugu rubrip
1271	55.5	12.0	194	1	TIM22_HUMAN	Q9y584	homo sapien
1272	55.5	12.0	196	1	CLPP1_PROMP	Q7v1w0	prochloroco

1273	55.5	12.0	198	2	Q87A07_XYLFT	Q87a07	xylella fas
1274	55.5	12.0	199	2	Q65D47_BACLD	Q65d47	bacillus li
1275	55.5	12.0	206	2	Q9SE77_BRAOL	Q9se77	brassica ol
1276	55.5	12.0	211	2	Q9NA02_9CRUS	Q9na02	daphnia mag
1277	55.5	12.0	213	2	Q9NAQ9_CAEEL	Q9naq9	caenorhabdi
1278	55.5	12.0	214	2	Q61ZW4_CAEBR	Q61zw4	caenorhabdi
1279	55.5	12.0	221	2	Q6CL37_KLULA	Q6cl37	kluyveromyc
1280	55.5	12.0	223	2	Q9DCP4_MOUSE	Q9dcp4	mus musculu
1281	55.5	12.0	232	2	Q8B5R5_9TOMB	Q8b5r5	beet black
1282	55.5	12.0	235	2	Q4LQA6_9BURK	Q4lqa6	burkholderi
1283	55.5	12.0	237	2	Q4I9H8_GIBZE	Q4i9h8	gibberella
1284	55.5	12.0	237	2	Q4ZQ49_PSESY	Q4zq49	pseudomonas
1285	55.5	12.0	237	2	Q885Y3_PSESM	Q885y3	pseudomonas
1286	55.5	12.0	240	2	Q8XW05_RALSO	Q8xw05	ralstonia s
1287	55.5	12.0	245	2	Q98R89_MYCPU	Q98r89	mycoplasma
1288	55.5	12.0	245	2	Q7ZYW1_BRARE	Q7zyw1	brachydanio
1289	55.5	12.0	248	2	Q6CA49_YARLI	Q6ca49	yarrowia li
1290	55.5	12.0	250	2	Q89L47_BRAJA	Q89l47	bradyrhizob
1291	55.5	12.0	253	2	Q7PJ20_ANOGA	Q7pj20	anopheles g
1292	55.5	12.0	253	2	Q8FP86_COREF	Q8fp86	corynebacte
1293	55.5	12.0	254	2	Q9RWP1_DEIRA	Q9rwp1	deinococcus
1294	55.5	12.0	256	2	Q9RUK4_DEIRA	Q9ruk4	deinococcus
1295	55.5	12.0	257	1	PEBB_PROMM	Q7v585	prochloroco
1296	55.5	12.0	262	1	BACR_HALSA	P02945	halobacteri
1297	55.5	12.0	262	2	Q5HLI2_STAEQ	Q5hli2	staphylococ
1298	55.5	12.0	262	2	Q4G5W6_BRARE	Q4g5w6	brachydanio
1299	55.5	12.0	263	2	Q5CVY7_CRYPV	Q5cvy7	cryptospori
1300	55.5	12.0	263	2	Q5CFK0_CRYHO	Q5cfk0	cryptospori
1301	55.5	12.0	270	2	Q5VU30_HUMAN	Q5vu30	homo sapien
1302	55.5	12.0	270	2	Q98866_BRARE	Q98866	brachydanio
1303	55.5	12.0	283	2	Q5V2V1_HALMA	Q5v2v1	haloarcula
1304	55.5	12.0	292	2	Q91XR2_CAVPO	Q91xr2	cavia porce
1305	55.5	12.0	295	2	Q6GNN7_XENLA	Q6gnn7	xenopus lae
1306	55.5	12.0	299	2	Q9HZ18_PSEAE	Q9hz18	pseudomonas
1307	55.5	12.0	300	2	Q5P736_AZOSE	Q5p736	azoarcus sp
1308	55.5	12.0	309	2	Q8DPP1_STRR6	Q8dpp1	streptococc
1309	55.5	12.0	309	2	Q97QL2_STRPN	Q97ql2	streptococc
1310	55.5	12.0	312	1	CATO_MOUSE	Q8bm88	mus musculu
1311	55.5	12.0	312	2	Q4QQL3_MOUSE	Q4qql3	mus musculu
1312	55.5	12.0	315	2	Q6LHU3_PHOPR	Q6lhu3	photobacter
1313	55.5	12.0	316	2	Q9RUA8_DEIRA	Q9rua8	deinococcus
1314	55.5	12.0	317	1	EXOZ_RHIME	P26502	rhizobium m
1315	55.5	12.0	323	2	Q888H6_PSESM	Q888h6	pseudomonas
1316	55.5	12.0	324	2	Q9BF59_ATEFU	Q9bf59	ateles fusc
1317	55.5	12.0	325	2	Q6LG58_PHOPR	Q6lg58	photobacter
1318	55.5	12.0	326	2	Q97CS8_THEVO	Q97cs8	thermoplasm
1319	55.5	12.0	326	2	Q9BF48_PIG	Q9bf48	sus scrofa
1320	55.5	12.0	326	2	Q9BF60_LEMCA	Q9bf60	lemur catta
1321	55.5	12.0	326	2	Q9BF72_SORAR	Q9bf72	sorex arane
1322	55.5	12.0	326	2	Q9BF75_MYRTR	Q9bf75	myrmecophag
1323	55.5	12.0	326	2	Q9BF76_TAMTE	Q9bf76	tamandua te
1324	55.5	12.0	326	2	Q99NQ7_AGOTA	Q99nq7	agouti tacz
1325	55.5	12.0	326	2	Q99NQ9_HYDHY	Q99nq9	hydrochoeru
1326	55.5	12.0	326	2	Q99NR0_9HYST	Q99nr0	cavia tschu
1327	55.5	12.0	326	2	Q99NR3_EREDO	Q99nr3	erethizon d
1328	55.5	12.0	326	2	Q99NR4_HYSBR	Q99nr4	hystrix bra
1329	55.5	12.0	326	2	Q99NR8_CASCN	Q99nr8	castor cana
1330	55.5	12.0	331	2	Q59NG1_CANAL	Q59ng1	candida alb
1331	55.5	12.0	331	2	Q5KPG4_CRYNE	Q5kpg4	cryptococcu
1332	55.5	12.0	336	2	Q4H4M1_9DEIO	Q4h4m1	deinococcus
1333	55.5	12.0	341	2	Q4H4Z8_9DEIO	Q4h4z8	deinococcus
1334	55.5	12.0	343	2	Q98865_BRARE	Q98865	brachydanio
1335	55.5	12.0	344	2	Q8YQ35_ANASP	Q8yq35	anabaena sp
1336	55.5	12.0	346	2	O59293_PYRHO	O59293	pyrococcus
1337	55.5	12.0	346	2	Q740N5_MYCPA	Q740n5	mycobacteri
1338	55.5	12.0	357	2	Q80LT8_NPVAH	Q80lt8	adoxophyes
1339	55.5	12.0	358	2	Q67TC7_SYMTH	Q67tc7	symbiobacte
1340	55.5	12.0	376	1	OE56_NPVAC	P41705	autographa
1341	55.5	12.0	378	2	Q8B9B5_NPVRO	Q8b9b5	rachiplusia
1342	55.5	12.0	379	1	OE56_NPVCF	P41718	choristoneu
1343	55.5	12.0	379	2	Q882F2_PSESM	Q882f2	pseudomonas
1344	55.5	12.0	379	2	Q77DF6_NPVCF	Q77df6	choristoneu
1345	55.5	12.0	381	2	Q82B18_STRAW	Q82b18	streptomyce
1346	55.5	12.0	382	2	Q5BIP0_BOVIN	Q5bip0	bos taurus
1347	55.5	12.0	383	1	YJK8_YEAST	P42946	saccharomyc
1348	55.5	12.0	383	2	Q6Q5N7_YEAST	Q6q5n7	saccharomyc
1349	55.5	12.0	383	2	Q5Z0K5_NOCFA	Q5z0k5	nocardia fa
1350	55.5	12.0	384	2	Q9LL38_BRANA	Q9ll38	brassica na
1351	55.5	12.0	384	2	Q9LIA9_ARATH	Q9lia9	arabidopsis
1352	55.5	12.0	385	2	Q9FX15_ARATH	Q9fx15	arabidopsis
1353	55.5	12.0	389	2	Q6PQJ8_DIGPU	Q6pqj8	digitalis p
1354	55.5	12.0	389	2	Q5HV30_CAMJR	Q5hv30	campylobact
1355	55.5	12.0	389	2	Q9PPF7_CAMJE	Q9ppf7	campylobact
1356	55.5	12.0	393	2	Q4NU11_9DELT	Q4nu11	anaeromyxob
1357	55.5	12.0	394	2	Q560G3_CRYNE	Q560g3	cryptococcu
1358	55.5	12.0	407	2	Q947C6_TRIMO	Q947c6	triticum mo
1359	55.5	12.0	409	2	Q4NRD2_9DELT	Q4nrd2	anaeromyxob
1360	55.5	12.0	414	2	Q7MHX0_VIBVY	Q7mhx0	vibrio vuln
1361	55.5	12.0	417	2	Q9ZIS3_ECOLI	Q9zis3	escherichia
1362	55.5	12.0	425	2	Q5WRV3_LEGPL	Q5wrv3	legionella
1363	55.5	12.0	425	2	Q5WXT6_LEGPL	Q5wxt6	legionella
1364	55.5	12.0	425	2	Q5X6C6_LEGPA	Q5x6c6	legionella
1365	55.5	12.0	431	2	Q9MS90_9MAGN	Q9ms90	austrobaile
1366	55.5	12.0	437	2	Q83CE5_COXBU	Q83ce5	coxiella bu
1367	55.5	12.0	451	2	Q4NWM3_9DELT	Q4nwm3	anaeromyxob
1368	55.5	12.0	452	2	Q8KAS7_CHLTE	Q8kas7	chlorobium
1369	55.5	12.0	456	2	Q20523_CAEEL	Q20523	caenorhabdi
1370	55.5	12.0	459	2	Q9CIK1_LACLA	Q9cik1	lactococcus
1371	55.5	12.0	470	2	Q7MSR1_WOLSU	Q7msr1	wolinella s
1372	55.5	12.0	471	2	Q5FT20_GLUOX	Q5ft20	gluconobact
1373	55.5	12.0	483	2	Q9I829_ONCMY	Q9i829	oncorhynchu
1374	55.5	12.0	484	2	Q4ZCR7_9VIRU	Q4zcr7	bacteriopha
1375	55.5	12.0	484	2	Q73RS3_TREDE	Q73rs3	treponema d
1376	55.5	12.0	484	2	Q8NWL7_STAAW	Q8nwl7	staphylococ
1377	55.5	12.0	516	2	Q5JBE0_9LILI	Q5jbe0	toxicoscord
1378	55.5	12.0	522	2	Q8D5Q2_VIBVU	Q8d5q2	vibrio vuln
1379	55.5	12.0	522	2	Q7MCQ9_VIBVY	Q7mcq9	vibrio vuln
1380	55.5	12.0	528	2	Q73KN8_TREDE	Q73kn8	treponema d
1381	55.5	12.0	528	2	Q4RJ06_TETNG	Q4rj06	tetraodon n
1382	55.5	12.0	529	2	Q5CP72_CRYHO	Q5cp72	cryptospori
1383	55.5	12.0	545	2	Q8YPL8_ANASP	Q8ypl8	anabaena sp
1384	55.5	12.0	545	2	Q9PXA4_9PARA	Q9pxa4	measles vir
1385	55.5	12.0	546	2	Q91HA5_9PARA	Q91ha5	rinderpest
1386	55.5	12.0	553	2	O11380_9PARA	O11380	measles vir
1387	55.5	12.0	562	1	Y3471_BRAJA	Q89pk9	bradyrhizob
1388	55.5	12.0	566	2	Q5H4R5_XANOR	Q5h4r5	xanthomonas
1389	55.5	12.0	572	2	Q5R773_PONPY	Q5r773	pongo pygma
1390	55.5	12.0	580	2	Q98DA6_RHILO	Q98da6	rhizobium l
1391	55.5	12.0	587	2	Q9FK05_ARATH	Q9fk05	arabidopsis
1392	55.5	12.0	595	2	Q5R5H6_PONPY	Q5r5h6	pongo pygma
1393	55.5	12.0	596	2	Q7NJ84_GLOVI	Q7nj84	gloeobacter
1394	55.5	12.0	607	2	Q9C9Y1_ARATH	Q9c9y1	arabidopsis
1395	55.5	12.0	625	1	KCNC4_RAT	Q63734	rattus norv
1396	55.5	12.0	628	1	KCNC4_MOUSE	Q8r1c0	mus musculu
1397	55.5	12.0	631	2	Q7VND5_HAEDU	Q7vnd5	haemophilus
1398	55.5	12.0	631	2	Q803A6_BRARE	Q803a6	brachydanio
1399	55.5	12.0	634	2	Q961J0_DROME	Q961j0	drosophila
1400	55.5	12.0	635	1	KCNC4_HUMAN	Q03721	homo sapien
1401	55.5	12.0	643	1	YKD6_CAEEL	Q03564	caenorhabdi
1402	55.5	12.0	648	1	PRIA_RICPR	Q9zd10	rickettsia
1403	55.5	12.0	662	1	HEPA_HHV6U	P52375	human herpe
1404	55.5	12.0	678	2	Q82E42_STRAW	Q82e42	streptomyce
1405	55.5	12.0	687	2	Q9BXR8_HUMAN	Q9bxr8	homo sapien
1406	55.5	12.0	698	2	Q84ZI0_ORYSA	Q84zi0	oryza sativ
1407	55.5	12.0	716	1	P5CS_ORYSA	O04226	o delta 1-p
1408	55.5	12.0	716	2	Q6PW76_ORYSA	Q6pw76	oryza sativ
1409	55.5	12.0	716	2	Q60EM4_ORYSA	Q60em4	oryza sativ
1410	55.5	12.0	726	2	Q8HTM8_9MAGN	Q8htm8	diphylleia
1411	55.5	12.0	740	2	Q8DJL7_SYNEL	Q8dj17	synechococc
1412	55.5	12.0	742	2	Q6MNV6_BDEBA	Q6mnv6	bdellovibri
1413	55.5	12.0	751	2	Q9AYM4_VIGUN	Q9aym4	vigna ungui
1414	55.5	12.0	788	2	Q6INE9_XENLA	Q6ine9	xenopus lae
1415	55.5	12.0	806	1	PA2G6_HUMAN	O60733	homo sapien
1416	55.5	12.0	806	2	Q7W7V0_BORPA	Q7w7v0	bordetella
1417	55.5	12.0	806	2	Q7WL90_BORBR	Q7wl90	bordetella
1418	55.5	12.0	806	2	Q7MP30_VIBVY	Q7mp30	vibrio vuln

1419	55.5	12.0	849	2	Q4RGD7_TETNG	Q4rgd7 tetraodon n
1420	55.5	12.0	880	2	Q4KM12_BRARE	Q4km12 brachydanio
1421	55.5	12.0	886	1	SEM6B_MOUSE	O54951 mus musculu
1422	55.5	12.0	887	1	SEM6B_RAT	O70141 rattus norv
1423	55.5	12.0	888	1	SEM6B_HUMAN	Q9h3t3 homo sapien
1424	55.5	12.0	893	1	DAG1_MOUSE	Q62165 mus musculu
1425	55.5	12.0	893	2	Q8BPJ7_MOUSE	Q8bpj7 mus musculu
1426	55.5	12.0	893	2	Q8CBE6_MOUSE	Q8cbe6 mus musculu
1427	55.5	12.0	893	2	Q544G5_MOUSE	Q544g5 mus musculu
1428	55.5	12.0	895	1	DAG1_BOVIN	O18738 bos taurus
1429	55.5	12.0	925	2	Q7XPE9_ORYSA	Q7xpe9 oryza sativ
1430	55.5	12.0	946	1	C1TC_YEAST	P07245 s c-1-tetra
1431	55.5	12.0	968	2	Q8TW58_METKA	Q8tw58 methanopyru
1432	55.5	12.0	1020	2	Q95XY4_CAEEL	Q95xy4 caenorhabdi
1433	55.5	12.0	1062	2	Q7QV26_GIALA	Q7qv26 giardia lam
1434	55.5	12.0	1104	2	Q7S728_NEUCR	Q7s728 neurospora
1435	55.5	12.0	1119	2	Q5BA79_EMENI	Q5ba79 aspergillus
1436	55.5	12.0	1131	2	Q6C011_YARLI	Q6c011 yarrowia li
1437	55.5	12.0	1148	2	Q54YC9_DICDI	Q54yc9 dictyosteli
1438	55.5	12.0	1217	2	O17889_CAEEL	O17889 caenorhabdi
1439	55.5	12.0	1423	1	FRUA_STRMU	Q03174 streptococc
1440	55.5	12.0	1453	2	Q7T6T3_9CORO	Q7t6t3 canine coro
1441	55.5	12.0	1469	2	Q4WTA3_ASPFU	Q4wta3 aspergillus
1442	55.5	12.0	1632	2	Q4S1D3_TETNG	Q4s1d3 tetraodon n
1443	55.5	12.0	1637	2	Q50Z97_ENTHI	Q50z97 entamoeba h
1444	55.5	12.0	1731	2	Q4QJ23_LEIMA	Q4qj23 leishmania
1445	55.5	12.0	1913	2	Q4Q986_LEIMA	Q4q986 leishmania
1446	55.5	12.0	2054	1	MPDZ_RAT	O55164 rattus norv
1447	55.5	12.0	2220	2	Q9GV40_DROME	Q9gv40 drosophila
1448	55.5	12.0	2236	2	Q9VCN1_DROME	Q9vcn1 drosophila
1449	55.5	12.0	4905	2	Q4FZ33_LEIMA	Q4fz33 leishmania
1450	55	11.9	52	2	O45059_CAEEL	O45059 caenorhabdi
1451	55	11.9	66	2	Q7U8Y3_SYNPX	Q7u8y3 synechococc
1452	55	11.9	92	2	Q4RYG8_TETNG	Q4ryg8 tetraodon n
1453	55	11.9	93	2	Q82Q38_STRAW	Q82q38 streptomyce
1454	55	11.9	94	2	Q85P51_9CUCU	Q85p51 otiorhynchu
1455	55	11.9	95	2	Q864R3_CANFA	Q864r3 canis famil
1456	55	11.9	123	2	Q6LGG8_PHOPR	Q6lgg8 photobacter
1457	55	11.9	128	1	Y070_TREPA	O83109 treponema p
1458	55	11.9	134	2	Q86ZV1_NEUCR	Q86zv1 neurospora
1459	55	11.9	159	2	Q5XD59_STRP6	Q5xd59 streptococc
1460	55	11.9	159	2	Q9A0V4_STRPY	Q9a0v4 streptococc
1461	55	11.9	159	2	Q7CNF4_STRP8	Q7cnf4 streptococc
1462	55	11.9	159	2	Q7CFB9_STRP3	Q7cfb9 streptococc
1463	55	11.9	160	1	PETD_GUITH	O78415 guillardia
1464	55	11.9	166	2	Q5QS55_PHATA	Q5qs55 phascogale
1465	55	11.9	178	1	CRCB2_BIFLO	Q8g5c3 bifidobacte
1466	55	11.9	190	2	Q6W3A0_9CREN	Q6w3a0 uncultured
1467	55	11.9	202	2	Q62KV1_BURMA	Q62kv1 burkholderi
1468	55	11.9	202	2	Q63TK1_BURPS	Q63tk1 burkholderi
1469	55	11.9	208	2	Q9PSA1_CHICK	Q9psa1 gallus gall
1470	55	11.9	212	2	Q8D874_VIBVU	Q8d874 vibrio vuln
1471	55	11.9	212	2	Q9KQG3_VIBCH	Q9kqg3 vibrio chol
1472	55	11.9	218	2	Q848N7_9BACT	Q848n7 uncultured
1473	55	11.9	220	2	Q84IE1_BACFR	Q84ie1 bacteroides
1474	55	11.9	223	2	Q9XCA4_PORGI	Q9xca4 porphyromon
1475	55	11.9	225	2	Q9BRQ7_HUMAN	Q9brq7 homo sapien
1476	55	11.9	228	2	Q83UY3_LISMO	Q83uy3 listeria mo
1477	55	11.9	228	2	Q63R53_BURPS	Q63r53 burkholderi
1478	55	11.9	228	2	Q62HE2_BURMA	Q62he2 burkholderi
1479	55	11.9	229	2	Q83TM3_LISMO	Q83tm3 listeria mo
1480	55	11.9	229	2	Q83UH3_LISMO	Q83uh3 listeria mo
1481	55	11.9	235	2	Q8NC40_HUMAN	Q8nc40 homo sapien
1482	55	11.9	235	2	Q7MM99_VIBVY	Q7mm99 vibrio vuln
1483	55	11.9	242	2	Q9BSV0_HUMAN	Q9bsv0 homo sapien
1484	55	11.9	252	2	Q6IUV0_PODAN	Q6iuv0 podospora a
1485	55	11.9	252	2	Q7TNC3_MOUSE	Q7tnc3 mus musculu
1486	55	11.9	253	2	Q63IQ1_BURPS	Q63iq1 burkholderi
1487	55	11.9	255	2	Q8TUS5_METKA	Q8tus5 methanopyru
1488	55	11.9	263	2	Q8GFE8_STRAU	Q8gfe8 streptomyce
1489	55	11.9	263	2	Q79RD6_FRATT	Q79rd6 francisella
1490	55	11.9	264	2	Q6Z386_ORYSA	Q6z386 oryza sativ
1491	55	11.9	265	2	Q7P1L4_CHRVO	Q7p1l4 chromobacte
1492	55	11.9	268	1	EA30_VICFA	P21745 vicia faba
1493	55	11.9	268	2	Q43675_VICFA	Q43675 vicia faba
1494	55	11.9	270	2	O94006_CANAL	O94006 candida alb
1495	55	11.9	270	2	Q5A4M8_CANAL	Q5a4m8 candida alb
1496	55	11.9	270	2	Q8BY39_MOUSE	Q8by39 mus musculu
1497	55	11.9	273	2	Q73NN2_TREDE	Q73nn2 treponema d
1498	55	11.9	275	2	Q54KD4_DICDI	Q54kd4 dictyosteli
1499	55	11.9	277	2	Q9FYE3_ARATH	Q9fye3 arabidopsis
1500	55	11.9	282	2	Q9Y4U1_HUMAN	Q9y4u1 homo sapien

ALIGNMENTS

```
RESULT 1
Q6UWZ1_HUMAN
ID   Q6UWZ1_HUMAN PRELIMINARY;      PRT;    89 AA.
AC   Q6UWZ1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   ERVT526.
GN   Name=FXYD4; ORFNames=UNQ526;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AY358584; AAQ88947.1; -; mRNA.
DR   HGNC; HGNC:4028; FXYD4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0006811; P:ion transport; IEA.
DR   InterPro; IPR000272; FXYD.
DR   Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR   PROSITE; PS01310; FXYD; 1.
SQ   SEQUENCE   89 AA;  9433 MW;  C5934288182449B0 CRC64;

  Query Match           100.0%;  Score 461;  DB 2;  Length 89;
  Best Local Similarity  100.0%;  Pred. No. 3e-41;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60

Qy         61 CKYKSSQKQHSPVPEKAIPLITPGSATTC 89
              |||||||||||||||||||||||||||||
Db         61 CKYKSSQKQHSPVPEKAIPLITPGSATTC 89


RESULT 2
Q7Z4M5_HUMAN
ID   Q7Z4M5_HUMAN PRELIMINARY;      PRT;    89 AA.
AC   Q7Z4M5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
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DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   FXYD domain containing ion transport regulator 4.
GN   Name=FXYD4; ORFNames=RP11-92P6.2-004;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Corby N.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC054876; AAH54876.1; -; mRNA.
DR   EMBL; AL512654; CAI17065.1; -; Genomic_DNA.
DR   Ensembl; ENSG00000150201; Homo sapiens.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0006811; P:ion transport; IEA.
DR   InterPro; IPR000272; FXYD.
DR   Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR   PROSITE; PS01310; FXYD; 1.
SQ   SEQUENCE   89 AA;  9373 MW;  C5935929A22449B0 CRC64;

  Query Match             98.0%;  Score 452;  DB 2;  Length 89;
  Best Local Similarity   98.9%;  Pred. No. 2.7e-40;
  Matches   88;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60

Qy         61 CKYKSSQKQHSPVPEKAIPLITPGSATTC 89
              || |||||||||||||||||||||||||||
Db         61 CKCKSSQKQHSPVPEKAIPLITPGSATTC 89


RESULT 3
FXYD4_HUMAN
ID   FXYD4_HUMAN    STANDARD;      PRT;    89 AA.
AC   P59646;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   FXYD domain-containing ion transport regulator 4 precursor.
GN   Name=FXYD4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION.
RX   MEDLINE=20408885; PubMed=10950925; DOI=10.1006/geno.2000.6274;
RA   Sweadner K.J., Rael E.;
RT   "The FXYD gene family of small ion transport regulators or channels:
RT   cDNA sequence, protein signature sequence, and expression.";
RL   Genomics 68:41-56(2000).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the FXYD family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AI829935; -; NOT_ANNOTATED_CDS; mRNA.
DR   Ensembl; ENSG00000150201; Homo sapiens.
DR   HGNC; HGNC:4028; FXYD4.
DR   InterPro; IPR000272; FXYD.
DR   Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR   PROSITE; PS01310; FXYD; 1.
KW   Ion transport; Ionic channel; Signal; Transmembrane; Transport.
FT   SIGNAL        1     20       Potential.
FT   CHAIN        21     89       FXYD domain-containing ion transport
FT                                regulator 4.
FT   TOPO_DOM     21     38       Extracellular (Potential).
FT   TRANSMEM     39     59       Potential.
FT   TOPO_DOM     60     89       Cytoplasmic (Potential).
SQ   SEQUENCE   89 AA;  9373 MW;  B595EF99A49449B4 CRC64;

  Query Match             97.6%;  Score 450;  DB 1;  Length 89;
  Best Local Similarity   97.8%;  Pred. No. 4.5e-40;
  Matches   87;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MERVTLALLILAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60

Qy         61 CKYKSSQKQHSPVPEKAIPLITPGSATTC 89
              || |||||||||||||||||||||||||||
Db         61 CKCKSSQKQHSPVPEKAIPLITPGSATTC 89
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RESULT 4
FXYD4_MOUSE
ID   FXYD4_MOUSE    STANDARD;      PRT;    88 AA.
AC   Q9D2W0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   FXYD domain-containing ion transport regulator 4 precursor (Channel
DE   inducing factor) (CHIF).
GN   Name=Fxyd4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/SvJ;
RA   Garty H.;
RT   "Genomic sequence of mouse CHIF (FXYD4).";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the FXYD family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF362729; AAK51508.1; -; Genomic_DNA.
DR   EMBL; AK018728; BAB31372.1; -; mRNA.
DR   EMBL; BC086918; AAH86918.1; -; mRNA.
DR   Ensembl; ENSMUSG00000004988; Mus musculus.
DR   MGI; MGI:1889005; Fxyd4.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   InterPro; IPR000272; FXYD.
DR   Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR   PROSITE; PS01310; FXYD; 1.
KW   Ion transport; Ionic channel; Signal; Transmembrane; Transport.
FT   SIGNAL        1     20       Potential.
FT   CHAIN        21     88       FXYD domain-containing ion transport
FT                                regulator 4.
FT   TOPO_DOM     21     38       Extracellular (Potential).
FT   TRANSMEM     39     59       Potential.
FT   TOPO_DOM     60     88       Cytoplasmic (Potential).
SQ   SEQUENCE   88 AA;  9269 MW;  7EB0140941CFE926 CRC64;

  Query Match             60.0%;  Score 276.5;  DB 1;  Length 88;
  Best Local Similarity   66.7%;  Pred. No. 1.4e-21;
  Matches   60;  Conservative    8;  Mismatches   19;  Indels    3;  Gaps    3;

Qy          1 MERVTLA-LLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              || :| | ||||||| ||||:||  :|| ||||||::||| ||| |||| ||||| |||
Db          1 MEEITCAFLLLLAGLPALEASDP-VDKDSPFYYDWESLQLGGLIFGGLLCIAGIAMALSG 59

Qy         60 KCKYKSSQKQHSPVPEKAIPLITPGSATTC 89
              ||| : : |  | :| || ||| |||| ||
Db         60 KCKCRRTHKP-SSLPGKATPLIIPGSANTC 88


RESULT 5
FXYD4_RAT
ID   FXYD4_RAT      STANDARD;      PRT;    87 AA.
AC   Q63113;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   FXYD domain-containing ion transport regulator 4 precursor (Channel
DE   inducing factor) (CHIF) (Corticosteroid-induced protein).
GN   Name=Fxyd4;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Wistar; TISSUE=Colon;
RX   MEDLINE=95320221; PubMed=7597086;
RA   Attali B., Latter H., Rachamim N., Garty H.;
RT   "A corticosteroid-induced gene expressing an 'IsK-like' K+ channel
RT   activity in Xenopus oocytes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:6092-6096(1995).
RN   [2]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=97000648; PubMed=8843704;
RA   Capurro C., Coutry N., Bonvalet J.-P., Escoubet B., Garty H.,
```

```
RA   Farman N.;
RT   "Cellular localization and regulation of CHIF in kidney and colon.";
RL   Am. J. Physiol. 271:C753-C762(1996).
CC   -!- FUNCTION: Induces a potassium channel when expressed in Xenopus
CC       oocytes.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Selectively present in the distal parts of the
CC       nephron (medullary and papillary collecting ducts and end portions
CC       of cortical collecting tubule) and in the epithelial cells of the
CC       distal colon. No expression is found in renal proximal tubule,
CC       loop of henle and distal tubule, proximal colon, small intestine,
CC       lung, choroid plexus, salivary glands, or brain.
CC   -!- INDUCTION: By corticosteroids.
CC   -!- SIMILARITY: Belongs to the FXYD family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; L41254; AAA74691.1; -; mRNA.
DR   PIR; I59391; I59391.
DR   Ensembl; ENSRNOG00000014578; Rattus norvegicus.
DR   RGD; 70998; Fxyd4.
DR   GO; GO:0005267; F:potassium channel activity; IDA.
DR   InterPro; IPR000272; FXYD.
DR   Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR   PROSITE; PS01310; FXYD; 1.
KW   Ion transport; Ionic channel; Signal; Transmembrane; Transport.
FT   SIGNAL        1     20       Potential.
FT   CHAIN        21     87       FXYD domain-containing ion transport
FT                                regulator 4.
FT   TOPO_DOM     21     38       Extracellular (Potential).
FT   TRANSMEM     39     59       Potential.
FT   TOPO_DOM     60     87       Cytoplasmic (Potential).
SQ   SEQUENCE   87 AA;  9084 MW;  5D0DE1FFC6B1BCCA CRC64;

  Query Match             55.6%;  Score 256.5;  DB 1;  Length 87;
  Best Local Similarity   61.5%;  Pred. No. 1.9e-19;
  Matches   56;  Conservative   11;  Mismatches   17;  Indels    7;  Gaps    4;

Qy          1 MERVTLA-LLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              || :| | ||:|||| |||| |  :|  ||||||::||| |:| |||| |||||  |||
Db          1 MEGITCAFLLVLAGLPVLEANGP-VDKGSPFYYDWESLQLGGMIFGGLLCIAGIAMALSG 59

Qy         60 KCKYKSSQKQHSP--VPEKAIPLITPGSATT 88
              |||    :: |:|  :|||  ||||||||:|
Db         60 KCK---CRRNHTPSSLPEKVTPLITPGSAST 87


RESULT 6
FXYD3_MOUSE
ID   FXYD3_MOUSE    STANDARD;      PRT;    88 AA.
AC   Q61835;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   FXYD domain-containing ion transport regulator 3 precursor (Chloride
DE   conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein)
DE   (Phospholemman-like).
GN   Name=Fxyd3; Synonyms=Mat8, Plml;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Mammary gland;
RX   MEDLINE=95060797; PubMed=7970700;
RA   Morrison B.W., Leder P.;
RT   "neu and ras initiate murine mammary tumors that share genetic markers
RT   generally absent in c-myc and int-2-initiated tumors.";
RL   Oncogene 9:3417-3426(1994).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   EXPRESSION.
RX   MEDLINE=95138184; PubMed=7836447; DOI=10.1074/jbc.270.15.8571;
RA   Morrison B.W., Moorman J.R., Kowdley G.C., Kobayashi Y.M., Jones L.R.,
RA   Leder P.;
RT   "Mat-8, a novel phospholemman-like protein expressed in human breast
RT   tumors, induces a chloride conductance in Xenopus oocytes.";
RL   J. Biol. Chem. 270:2176-2182(1995).
CC   -!- FUNCTION: Induces a hyperpolarization-activated chloride current
CC       when expressed in Xenopus oocytes. May be a modulator capable of
CC       activating endogenous oocyte channels.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Expressed in a subset of murine breast tumors.
CC   -!- MISCELLANEOUS: Marker of a cell type preferentially transformed by
CC       neu or ras oncoprotein.
CC   -!- SIMILARITY: Belongs to the FXYD family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X93038; CAA63606.1; -; mRNA.
DR   EMBL; BC002039; AAH02039.1; -; mRNA.
DR   EMBL; BC056223; AAH56223.1; -; mRNA.
DR   PIR; S61552; S61552.
DR   Ensembl; ENSMUSG00000057092; Mus musculus.
DR   MGI; MGI:107497; Fxyd3.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   InterPro; IPR000272; FXYD.
DR   Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR   PROSITE; PS01310; FXYD; 1.
KW   Chloride; Chloride channel; Ion transport; Ionic channel; Signal;
KW   Transmembrane; Transport.
FT   SIGNAL        1     20       Potential.
FT   CHAIN        21     88       FXYD domain-containing ion transport
FT                                regulator 3.
FT   TOPO_DOM     21     38       Extracellular (Potential).
FT   TRANSMEM     39     59       Potential.
FT   TOPO_DOM     60     88       Cytoplasmic (Potential).
SQ   SEQUENCE   88 AA;  9526 MW;  9CD61684B856E35D CRC64;

  Query Match             52.4%;  Score 241.5;  DB 1;  Length 88;
  Best Local Similarity   57.8%;  Pred. No. 7.5e-18;
  Matches   52;  Conservative   11;  Mismatches   24;  Indels    3;  Gaps    3;
```

```
Qy          1 MERVTLALL-LLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              |: | |:|| |||||  |:||||  ||:||||||| :|:: |||| |:|   ||  ::||
Db          1 MQEVVLSLLVLLAGLPTLDANDP-ENKNDPFYYDWYSLRVGGLICAGILCALGIIVLMSG 59

Qy         60 KCKYKSSQKQHSPVPEKAIPLITPGSATTC 89
              ||| |  ||  |  | :  ||||||||  |
Db         60 KCKCKFRQKP-SHRPGEGPPLITPGSAHNC 88


RESULT 7
FXYD3_RAT
ID   FXYD3_RAT      STANDARD;      PRT;    88 AA.
AC   P59645;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   FXYD domain-containing ion transport regulator 3 precursor.
GN   Name=Fxyd3;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lee N.H., Glodek A., Chandra I., Mason T.M., Quackenbush J.,
RA   Kerlavage A.R., Adams M.D.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION.
RX   MEDLINE=20408885; PubMed=10950925; DOI=10.1006/geno.2000.6274;
RA   Sweadner K.J., Rael E.;
RT   "The FXYD gene family of small ion transport regulators or channels:
RT   cDNA sequence, protein signature sequence, and expression.";
RL   Genomics 68:41-56(2000).
CC   -!- FUNCTION: Induces a hyperpolarization-activated chloride current
CC       when expressed in Xenopus oocytes. May be a modulator capable of
CC       activating endogenous oocyte channels.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the FXYD family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AA801365; -; NOT_ANNOTATED_CDS; mRNA.
DR   Ensembl; ENSRNOG00000021095; Rattus norvegicus.
DR   InterPro; IPR000272; FXYD.
DR   Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR   PROSITE; PS01310; FXYD; 1.
KW   Ion transport; Ionic channel; Signal; Transmembrane; Transport.
FT   SIGNAL        1     20       Potential.
FT   CHAIN        21     88       FXYD domain-containing ion transport
FT                                regulator 3.
FT   TOPO_DOM     21     38       Extracellular (Potential).
FT   TRANSMEM     39     59       Potential.
FT   TOPO_DOM     60     88       Cytoplasmic (Potential).
SQ   SEQUENCE   88 AA;  9411 MW;  45AFE872FD1AF944 CRC64;

  Query Match             50.9%;  Score 234.5;  DB 1;  Length 88;
  Best Local Similarity   56.7%;  Pred. No. 4.2e-17;
  Matches   51;  Conservative   10;  Mismatches   26;  Indels    3;  Gaps    3;

Qy          1 MERVTLALL-LLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              |:   |:|| |||||  |:||||  :|| |||||| :|:: |||| |:|   ||  ::||
Db          1 MQEFALSLLVLLAGLPTLDANDP-EDKDSPFYYDWHSLRVGGLICAGILCALGIIVLMSG 59

Qy         60 KCKYKSSQKQHSPVPEKAIPLITPGSATTC 89
              ||| | |||  |  |    ||||||||  |
Db         60 KCKCKFSQKP-SHRPGDGPPLITPGSAHNC 88


RESULT 8
FXYD3_PIG
ID   FXYD3_PIG      STANDARD;      PRT;    88 AA.
AC   O97797;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   FXYD domain-containing ion transport regulator 3 precursor (Chloride
DE   conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein).
GN   Name=FXYD3; Synonyms=MAT8;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Gastric mucosa;
RX   MEDLINE=99140476; PubMed=10206733;
RA   Maeda M., Hamano K., Hirano Y., Suzuki M., Takahashi E.-I., Terada T.,
RA   Futai M., Sato R.;
RT   "Structures of P-type transporting ATPases and chromosomal locations
RT   of their genes.";
RL   Cell Struct. Funct. 23:315-323(1998).
CC   -!- FUNCTION: Induces a hyperpolarization-activated chloride current
CC       when expressed in Xenopus oocytes. May be a modulator capable of
CC       activating endogenous oocyte channels.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the FXYD family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AB015759; BAA35078.1; -; mRNA.
DR   InterPro; IPR000272; FXYD.
DR   Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR   PROSITE; PS01310; FXYD; 1.
KW   Chloride; Chloride channel; Ion transport; Ionic channel; Signal;
KW   Transmembrane; Transport.
FT   SIGNAL        1     17       Potential.
FT   CHAIN        18     88       FXYD domain-containing ion transport
FT                                regulator 3.
FT   TOPO_DOM     18     38       Extracellular (Potential).
FT   TRANSMEM     39     59       Potential.
FT   TOPO_DOM     60     88       Cytoplasmic (Potential).
SQ   SEQUENCE   88 AA;  9314 MW;  6CC7810B90512E5A CRC64;

  Query Match             50.0%;  Score 230.5;  DB 1;  Length 88;
  Best Local Similarity   57.8%;  Pred. No. 1.1e-16;
  Matches   52;  Conservative   10;  Mismatches   25;  Indels    3;  Gaps    3;

Qy          1 MERVTLA-LLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              |  | |: |:|||||:||:||||  :|: ||||||  :|:: |||| |     ||  :|||
Db          1 MHEVALSVLILLAGLSALDANDP-EDKNSPFYYDWHSLRVGGLICAGTPCALGIIILLSG 59

Qy         60 KCKYKSSQKQHSPVPEKAIPLITPGSATTC 89
              ||| | |||  |  |  | |||||||  |
Db         60 KCKCKFSQKP-SHRPGDAPPLITPGSAHDC 88


RESULT 9
FXYD3_HUMAN
ID   FXYD3_HUMAN    STANDARD;      PRT;    87 AA.
AC   Q14802; Q13211;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   FXYD domain-containing ion transport regulator 3 precursor (Chloride
```

```
DE   conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein)
DE   (Phospholemman-like).
GN   Name=FXYD3; Synonyms=MAT8, PLML;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=95138184; PubMed=7836447; DOI=10.1074/jbc.270.15.8571;
RA   Morrison B.W., Moorman J.R., Kowdley G.C., Kobayashi Y.M., Jones L.R.,
RA   Leder P.;
RT   "Mat-8, a novel phospholemman-like protein expressed in human breast
RT   tumors, induces a chloride conductance in Xenopus oocytes.";
RL   J. Biol. Chem. 270:2176-2182(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung carcinoma;
RA   Lei W., Wu M.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Urinary bladder;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Induces a hyperpolarization-activated chloride current
CC       when expressed in Xenopus oocytes. May be a modulator capable of
CC       activating endogenous oocyte channels.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Expressed in a subset of human breast tumors.
CC   -!- MISCELLANEOUS: Marker of a cell type preferentially transformed by
CC       neu or ras oncoprotein.
CC   -!- SIMILARITY: Belongs to the FXYD family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X93036; CAA63604.1; -; mRNA.
DR   EMBL; U28249; AAA73922.1; -; mRNA.
DR   EMBL; BC005238; AAH05238.1; -; mRNA.
DR   PIR; A55571; A55571.
DR   Ensembl; ENSG00000089356; Homo sapiens.
DR   HGNC; HGNC:4027; FXYD3.
DR   H-InvDB; HIX0018290; -.
DR   MIM; 604996; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005254; F:chloride channel activity; TAS.
DR   GO; GO:0006821; P:chloride transport; TAS.
DR   InterPro; IPR000272; FXYD.
DR   Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR   PROSITE; PS01310; FXYD; 1.
KW   Chloride; Chloride channel; Ion transport; Ionic channel; Signal;
KW   Transmembrane; Transport.
FT   SIGNAL        1     20       Potential.
FT   CHAIN        21     87       FXYD domain-containing ion transport
FT                                regulator 3.
FT   TOPO_DOM     21     38       Extracellular (Potential).
FT   TRANSMEM     39     59       Potential.
FT   TOPO_DOM     60     87       Cytoplasmic (Potential).
FT   CONFLICT     36     37       Missing (in Ref. 2).
FT   CONFLICT     58     58       S -> SEWRSSGEQAGRGWGSPPLTTQLSPTG (in Ref.
FT                                2).
SQ   SEQUENCE   87 AA;  9263 MW;  6D674D668EB32493 CRC64;

  Query Match             46.5%;  Score 214.5;  DB 1;  Length 87;
  Best Local Similarity   54.5%;  Pred. No. 5.6e-15;
  Matches   48;  Conservative   11;  Mismatches   24;  Indels    5;  Gaps    4;

Qy          1 MERVTLALLL-LAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              |::||| ||: |||   |:|||   :|: |||||| :||: |||| |:|   ||  |:|
Db          1 MQKVTLGLLVFLAGFPVLDAND-LEDKNSPFYYDWHSLQVGGLICAGVLCAMGIIIVMSA 59

Qy         60 KCKYKSSQKQ-HSPVPEKAIPLITPGSA 86
              ||| |  ||  |   | :  ||||||||
Db         60 KCKCKFGQKSGHH--PGETPPLITPGSA 85


RESULT 10
Q6IB59_HUMAN
ID   Q6IB59_HUMAN PRELIMINARY;      PRT;    87 AA.
AC   Q6IB59;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   FXYD3 protein (FXYD domain containing ion transport regulator 3,
DE   isoform 1).
GN   Name=FXYD3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
RA   Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA   Korn B., Zuo D., Hu Y., LaBaer J.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=White Matter pool- 5 brain tissues- femoral artery;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=White Matter pool- 5 brain tissues- femoral artery;
RA   Director MGC Project;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR456945; CAG33226.1; -; mRNA.
DR   EMBL; CR542197; CAG46994.1; -; mRNA.
DR   EMBL; BT006712; AAP35358.1; -; mRNA.
DR   EMBL; BC090044; AAH90044.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0006811; P:ion transport; IEA.
DR   InterPro; IPR000272; FXYD.
DR   Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR   PROSITE; PS01310; FXYD; 1.
SQ   SEQUENCE   87 AA;  9263 MW;  6D674D668EB32493 CRC64;

  Query Match             46.5%;  Score 214.5;  DB 2;  Length 87;
  Best Local Similarity   54.5%;  Pred. No. 5.6e-15;
  Matches   48;  Conservative   11;  Mismatches   24;  Indels    5;  Gaps    4;

Qy          1 MERVTLALLL-LAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              |::||| ||: |||   |:|||   :|: |||||| :||: |||| |:|   ||  |:|
Db          1 MQKVTLGLLVFLAGFPVLDAND-LEDKNSPFYYDWHSLQVGGLICAGVLCAMGIIIVMSA 59

Qy         60 KCKYKSSQKQ-HSPVPEKAIPLITPGSA 86
              ||| |  ||  |   | :  ||||||||
Db         60 KCKCKFGQKSGHH--PGETPPLITPGSA 85


RESULT 11
Q80UV3_MOUSE
ID   Q80UV3_MOUSE PRELIMINARY;      PRT;    70 AA.
AC   Q80UV3;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fxyd3 protein.
GN   Name=Fxyd3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N;
RC   TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC   virgin mouse. Taken by biopsy.;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N;
RC   TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC   virgin mouse. Taken by biopsy.;
RG   NIH MGC Project;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC051033; AAH51033.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0006811; P:ion transport; IEA.
DR   InterPro; IPR000272; FXYD.
DR   Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR   PROSITE; PS01310; FXYD; 1.
SQ   SEQUENCE   70 AA;  7773 MW;  AB2A5EAF1490BF08 CRC64;

  Query Match             44.0%;  Score 203;  DB 2;  Length 70;
  Best Local Similarity   59.4%;  Pred. No. 7.6e-14;
  Matches   41;  Conservative   10;  Mismatches   16;  Indels    2;  Gaps    2;

Qy          1 MERVTLALL-LLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
              |: | |:|| |||||  |:|||| ||:||||||| :|:: |||| |:|   ||  ::||
Db          1 MQEVVLSLLVLLAGLPTLDANDP-ENKNDPFYYDWYSLRVGGLICAGILCALGIIVLMSG 59

Qy         60 KCKYKSSQK 68
              ||| |  ||
Db         60 KCKCKFRQK 68


RESULT 12
PLM_HUMAN
ID   PLM_HUMAN      STANDARD;      PRT;    92 AA.
AC   O00168;
DT   15-JUL-1998 (Rel. 36, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Phospholemman precursor (FXYD domain-containing ion transport
DE   regulator 1).
GN   Name=FXYD1; Synonyms=PLM;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Heart;
RX   MEDLINE=97312702; PubMed=9169143; DOI=10.1006/geno.1997.4665;
RA   Chen L.-S.K., Lo C.F., Numann R., Cuddy M.;
RT   "Characterization of the human and rat phospholemman (PLM) cDNAs and
RT   localization of the human PLM gene to chromosome 19q13.1.";
RL   Genomics 41:435-443(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20408885; PubMed=10950925; DOI=10.1006/geno.2000.6274;
RA   Sweadner K.J., Rael E.;
RT   "The FXYD gene family of small ion transport regulators or channels:
RT   cDNA sequence, protein signature sequence, and expression.";
RL   Genomics 68:41-56(2000).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain, Lung, and Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Induces a hyperpolarization-activated chloride current
CC       when expressed in Xenopus oocytes. May have a functional role in
CC       muscle contraction.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Highest expression in skeletal muscle and
CC       heart. Moderate levels in brain, placenta, lung, liver, pancreas,
CC       uterus, bladder, prostate, small intestine and colon with mucosal
CC       lining. Very low levels in kidney, colon and small intestine
CC       without mucosa, prostate without endothelial lining, spleen, and
CC       testis.
CC   -!- PTM: Major plasma membrane substrate for cAMP-dependent protein
CC       kinase (PK-A) and protein kinase C (PK-C) in several different
CC       tissues (By similarity). Phosphorylated in response to insulin and
CC       adrenergic stimulation.
CC   -!- SIMILARITY: Belongs to the FXYD family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U72245; AAC51286.1; -; mRNA.
DR   EMBL; BC032800; AAH32800.1; -; mRNA.
DR   Ensembl; ENSG00000126258; Homo sapiens.
DR   HGNC; HGNC:4025; FXYD1.
DR   MIM; 602359; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; NAS.
DR   GO; GO:0005254; F:chloride channel activity; TAS.
DR   GO; GO:0006821; P:chloride transport; TAS.
DR   GO; GO:0006936; P:muscle contraction; TAS.
DR   InterPro; IPR000272; FXYD.
DR   Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR   PROSITE; PS01310; FXYD; 1.
KW   Chloride; Chloride channel; Ion transport; Ionic channel;
KW   Phosphorylation; Signal; Transmembrane; Transport.
FT   SIGNAL       1     20       By similarity.
FT   CHAIN       21     92       Phospholemman.
FT   TOPO_DOM    21     35       Extracellular (Potential).
FT   TRANSMEM    36     56       Potential.
FT   TOPO_DOM    57     92       Cytoplasmic (Potential).
FT   MOD_RES     83     83       Phosphoserine (by PKA and PKC).
FT   MOD_RES     88     88       Phosphoserine (by PKA).
FT   CONFLICT     3      3       S -> P (in Ref. 1).
FT   CONFLICT     5      5       G -> H (in Ref. 1).
SQ   SEQUENCE   92 AA;  10441 MW;  11602EFEAFFD8BD8 CRC64;

  Query Match             28.0%;  Score 129;  DB 1;  Length 92;
  Best Local Similarity   41.3%;  Pred. No. 7.8e-06;
  Matches   26;  Conservative   15;  Mismatches   20;  Indels    2;  Gaps    1;

Qy         14 LTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKSSQKQHSPV 73
              ||  :|  |   : ||| ||:::||: ||:  |:| | ||  ||| :|: | :|:| :
Db         15 LTMAKAESP--KEHDPFTYDYQSLQIGGLVIAGILFILGILIVLSRRCRCKFNQQQRTGE 72

Qy         74 PEK 76
              |::
Db         73 PDE 75


RESULT 13
Q4RFG2_TETNG
ID   Q4RFG2_TETNG PRELIMINARY;      PRT;    88 AA.
AC   Q4RFG2;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 8 SCAF15119, whole genome shotgun sequence.
GN   ORFNames=GSTENG00035334001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01015119; CAG12870.1; -; Genomic_DNA.
SQ   SEQUENCE   88 AA;  9614 MW;  7067B36D3574AA13 CRC64;

  Query Match             27.7%;  Score 127.5;  DB 2;  Length 88;
  Best Local Similarity   43.3%;  Pred. No. 1.1e-05;
  Matches   29;  Conservative   13;  Mismatches   20;  Indels    5;  Gaps    2;

Qy          5 TLALLL--LAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK 62
              | ||||  || | | | : |   :|||| :|:  |:: |||   :| : ||  :|||:|:
Db          4 TCALLLMTLASLAAAEEHSP---EDDPFTFDYHRLRVGGLILAAVLCLIGIMILLSGRCR 60

Qy         63 YKSSQKQ 69
                | :| :
Db         61 CKFNQNK 67


RESULT 14
PLM_CANFA
ID   PLM_CANFA      STANDARD;      PRT;    92 AA.
AC   P56513;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Phospholemman precursor (FXYD domain-containing ion transport
DE   regulator 1).
GN   Name=FXYD1; Synonyms=PLM;
OS   Canis familiaris (Dog).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], AND PROTEIN SEQUENCE OF 21-92.
RC   TISSUE=Heart ventricle;
RX   MEDLINE=91250422; PubMed=1710217;
RA   Palmer C.J., Scott B.T., Jones L.R.;
RT   "Purification and complete sequence determination of the major plasma
RT   membrane substrate for cAMP-dependent protein kinase and protein
RT   kinase C in myocardium.";
RL   J. Biol. Chem. 266:11126-11130(1991).
CC   -!- FUNCTION: Induces a hyperpolarization-activated chloride current
CC       when expressed in Xenopus oocytes. May have a functional role in
CC       muscle contraction.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Present in heart, esophagus, stomach, aorta,
CC       skeletal muscle, smooth muscle, and liver but absent from brain
CC       and kidney.
CC   -!- PTM: Major plasma membrane substrate for cAMP-dependent protein
CC       kinase (PK-A) and protein kinase C (PK-C) in several different
CC       tissues. Phosphorylated in response to insulin and adrenergic
CC       stimulation (By similarity).
CC   -!- SIMILARITY: Belongs to the FXYD family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M63934; -; NOT_ANNOTATED_CDS; mRNA.
DR   PIR; A40533; A40533.
DR   InterPro; IPR000272; FXYD.
DR   Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR   PROSITE; PS01310; FXYD; 1.
KW   Chloride; Chloride channel; Direct protein sequencing; Ion transport;
KW   Ionic channel; Phosphorylation; Signal; Transmembrane; Transport.
FT   SIGNAL        1     20
FT   CHAIN        21     92       Phospholemman.
FT   TOPO_DOM     21     35       Extracellular (Potential).
FT   TRANSMEM     36     56       Potential.
FT   TOPO_DOM     57     92       Cytoplasmic (Potential).
FT   MOD_RES      83     83       Phosphoserine (by PKA and PKC) (By
FT                                similarity).
FT   MOD_RES      88     88       Phosphoserine (by PKA) (By similarity).
SQ   SEQUENCE   92 AA;  10500 MW;  890DE301BF8E740A CRC64;

  Query Match             27.4%;  Score 126.5;  DB 1;  Length 92;
  Best Local Similarity   41.4%;  Pred. No. 1.4e-05;
  Matches   29;  Conservative   15;  Mismatches   23;  Indels    3;  Gaps    2;

Qy          8 LLLLAG-LTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKSS 66
              |:|  | ||   |  |   : ||| ||:::|:: |||  |:| | ||  ||| :|: | :
Db          8 LVLCVGFLTTATAEAP--QEHDPFTYDYQSLRIGGLIIAGILFILGILIVLSRRCRCKFN 65

Qy         67 QKQHSPVPEK 76
              |:| :  |::
Db         66 QQQRTGEPDE 75


RESULT 15
FXYD6_RAT
ID   FXYD6_RAT      STANDARD;      PRT;    94 AA.
AC   Q91XV6; Q9JLR4;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   FXYD domain-containing ion transport regulator 6 precursor (Vascular
DE   endothelial cell specific protein 6) (VESP6) (Phosphohippolin).
GN   Name=Fxyd6; Synonyms=Php;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Liver;
RA   Aoki T., Toyoda H., Nishimoto S., Tawara J., Komurasaki T.;
RT   "Identification of VESP6,a vascular endothelial cell specific
RT   protein.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC   STRAIN=Sprague-Dawley; TISSUE=Hippocampus;
RX   MEDLINE=21105932; PubMed=11165386; DOI=10.1016/S0169-328X(00)00213-8;
RA   Yamaguchi F., Yamaguchi K., Tai Y., Sugimoto K., Tokuda M.;
RT   "Molecular cloning and characterization of a novel phospholemman-like
RT   protein from rat hippocampus.";
RL   Brain Res. Mol. Brain Res. 86:189-192(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Lung;
RG   NIH - Mammalian Gene Collection (MGC) project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q91XV6-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q91XV6-2; Sequence=VSP_001586;
CC   -!- SIMILARITY: Belongs to the FXYD family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AB030908; BAB62242.1; -; mRNA.
DR   EMBL; AF142439; AAF66613.1; -; mRNA.
DR   EMBL; BC072528; AAH72528.1; -; mRNA.
DR   Ensembl; ENSRNOG00000016412; Rattus norvegicus.
DR   RGD; 69315; Fxyd6.
DR   InterPro; IPR000272; FXYD.
DR   Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR   PROSITE; PS01310; FXYD; 1.
KW   Alternative splicing; Ion transport; Ionic channel; Signal;
KW   Transmembrane; Transport.
FT   SIGNAL        1     17       Potential.
FT   CHAIN        18     94       FXYD domain-containing ion transport
FT                                regulator 6.
FT   TOPO_DOM     18     34       Extracellular (Potential).
FT   TRANSMEM     35     57       Potential.
FT   TOPO_DOM     58     94       Cytoplasmic (Potential).
FT   VARSPLIC     20     20       Missing (in isoform 2).
FT                                /FTId=VSP_001586.
FT   CONFLICT     65     65       N -> S (in Ref. 2).
SQ   SEQUENCE   94 AA;  10388 MW;  1C0D35FA0C572451 CRC64;

  Query Match             27.0%;  Score 124.5;  DB 1;  Length 94;
  Best Local Similarity   37.5%;  Pred. No. 2.4e-05;
  Matches   33;  Conservative   15;  Mismatches   37;  Indels    3;  Gaps    2;

Qy          1 MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60
              || | :   ||| :    | :    | ||||||:: |:: ||:   :|   ||  :|| :
Db          1 METVLILCSLLAPVVLASAAEKEKEK-DPFYYDYQTLRIGGLVFAVVLFSVGILLILSRR 59

Qy         61 CKYKSSQKQHSPVPEKA--IPLITPGSA 86
                ||   :||  :|  |:|    |||  :|
Db         60 CKCSFNQKPRAPGDEEAQVENLITTNAA 87
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Search completed: May 12, 2006, 21:25:14
Job time : 367 secs